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(54) Title: COMPOSITIONS AND USES FOR SENTRIN, A CELL-DEATH PROTECTING PROTEIN (57) Abstract Disclosed are compositions comprising a novel cell-death protecting protein, sentrin-1, and the gene which encodes it. Also disclosed are methods of making and using sentrin polypeptides and nucleic acid segments in various diagnostic and pharmaceutical applications. In a preferred embodiment, overexpression of sentrin-1 confers protection against both anti-Fas/APO-1 and TNF-induced apoptosis.		

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WD-40 - DERIVED PEPTIDES AND USES THEREOF

Field of the Invention

The present invention relates in general to compositions and methods of modulating the function of proteins involved in protein-protein interactions. It relates more specifically to modulating the function of a first protein of a pair of interacting proteins wherein a second protein of the pair contains a "WD-40" or " β -transducin" amino acid repeat motif.

10 Background Art

Many intracellular processes are carried out or regulated by multi-subunit protein complexes that become active or repressed by the association or dissociation of individual polypeptide subunits.

15 One such group or family of proteins is related to the β subunit of transducin. Members of this group are all at least somewhat homologous to the β -subunit of transducin at the amino acid level, and contain a varying number of repeats of a particular motif identified in β -transducin. The repeats have
20 been termed " β -transducin", or "WD-40" repeats (Fong, et al.).

Among the members of this protein family (Duronio, et al.) are the $G\beta$ subunits that couple many receptors to their intracellular effector molecules, $G\beta/\gamma$ subunits that anchor another protein kinase (the β -adrenergic receptor kinase, β ARK),
25 DNA binding proteins and yeast cell cycle proteins. All of these require a transient protein-protein interaction for their function. However, the sequences at the interface of these proteins and their partners have not been identified.

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30 throughout the specification:

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Disclosure of the Invention

The invention includes, in one aspect, a polypeptide
10 composition effective to alter the activity of a first protein,
such as protein kinase C, or β -adrenergic receptor kinase
(β ARK). The polypeptide blocks or inhibits an interaction, such
as a binding interaction, between the first protein and a second
protein containing a WD-40 region.

15 The polypeptide contains between 4 and 50 amino acids
whose sequence is the same as a sequence of the same length in
the WD-40 region of the second protein.

The polypeptide may block the binding of the first to
the second protein, or may be an agonist or antagonist of the
20 first protein. The WD-40 region preferably has an amino acid
sequence homologous or identical to the sequences defined by SEQ
ID NO:76-261.

In a second embodiment, the invention includes a
method of altering the activity of the first protein of the type
25 defined above. The method includes selecting a polypeptide
having between 4 and 50 amino acids whose sequence is the same
as a sequence of the same length in the WD-40 region of the
second protein, and contacting the polypeptide with the first
protein under conditions which allow the formation of a complex
30 between the polypeptide and the first protein, where this
interaction alters the activity of the first protein.

In one embodiment, the contacting is effective to
inhibit the interaction between the first and second proteins.
In another embodiment, the contacting is effective to stimulate
35 the activity of the first protein.

In still another embodiment, the contacting is
effective to inhibit the activity of the first protein.

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The polypeptide preferably has an amino acid sequence homologous or identical to the sequences defined by SEQ ID NO:76-261.

In a more specific aspect of the invention, the invention includes a polypeptide composition effective to alter the activity of protein kinase C, where the protein kinase C interacts with a second protein, and the second protein contains at least one WD-40 region. The polypeptide has between 4 and 50 amino acids whose sequence is the same as a sequence of the same length in the WD-40 region of the second protein.

In a preferred embodiment, the second protein is a receptor for activated protein kinase C, and has the sequence represented by SEQ ID NO:27.

In other specific embodiments, the polypeptide is (i) an agonist of protein kinase C, and the polypeptide has the sequence represented by SEQ ID NO:7; (ii) an antagonist of the activity of protein kinase C; and/or (iii) an inhibitor of the interaction between protein kinase C and the second protein. In the latter embodiment, the polypeptide has sequence corresponding to SEQ ID NO:4 or SEQ ID NO:7.

The WD-40 region preferably has an amino acid sequence homologous or identical to SEQ ID NO:69-75.

In a related embodiment, the invention includes a method of altering the activity of a protein kinase C that interacts with a second protein, where said second protein contains at least one WD-40 region.

The method includes selecting a polypeptide having between 4 and 50 amino acids whose sequence is the same as a sequence of the same length in the WD-40 region of the second protein, and contacting the polypeptide with the protein kinase C under conditions which allow the formation of a complex between the polypeptide and the protein kinase C, where said interaction alters the activity of said protein kinase C.

Other aspects of the invention include the polypeptide compositions of the invention wherein said polypeptide is coupled to a solid support, as well as a method to bind selectively said first protein which method comprises contacting a sample putatively containing said first protein with the

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polypeptide composition bound to solid support and removing any unbound components of the sample from said composition.

In still another aspect, the invention relates to a method to assess the interaction of a first protein with a polypeptide represented by an amino acid sequence contained in a second protein, wherein said second protein contains at least one WD-40 region, which method comprises contacting a sample containing said first protein with a polypeptide composition wherein the polypeptide has between 4 and 50 amino acids whose sequence is the same as the sequence of the same length in the WD-40 region of the second protein, and observing any interaction of the first protein with said polypeptide composition. The invention also concerns a method to assess the ability of a candidate compound to bind a first protein which method comprises contacting said first protein with a polypeptide composition which binds said first protein, wherein the polypeptide of said composition has between 4 and 50 amino acids whose sequence is the same as a sequence of the same length in a WD-40 region of a second protein which interacts with said first protein, in the presence and absence of said candidate compound; and measuring the binding of said polypeptide in the presence and in the absence of said candidate, wherein decreased binding of the polypeptide in the presence as opposed to the absence of said candidate indicates that said candidate binds to said first protein.

In still another aspect, the invention is directed to recombinant materials for the production of the polypeptides of the invention and methods for their production.

These and other objects and features of the invention will become more fully apparent when the following detailed description of the invention is read in conjunction with the accompanying drawings.

Brief Description of the Figures

Figure 1A shows the cDNA sequence of rat brain RACK1.
Figure 1B shows an amino acid self-homology matrix analysis of RACK1.

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Figure 1C shows the amino acid sequence of RACK1, aligned to show the seven WD-40 repeats represented in the molecule.

Figure 2 shows the results of an overlay assay to
5 detect PKC binding to immobilized RACK1 in the presence and absence of PKC activators.

Figure 3 shows the results of an overlay assay to detect PKC binding to immobilized RACK1 in the presence and absence of WD-40-derived peptides.

10 Figure 4 shows the results of an overlay assay to detect binding of β PKC to either peptide I (SEQ ID NO:1) or peptide rVI (SEQ ID NO:7) immobilized on nitrocellulose membranes under various conditions.

Figure 5A shows the effects of injecting peptides I
15 (SEQ ID NO:1) and rVI (SEQ ID NO:7) on PKC-mediated germinal vesicle breakdown (GVBD), a measure of insulin-induced oocyte maturation.

Figure 5B shows the effects of injecting peptides I (SEQ ID NO:1) and rVI (SEQ ID NO:7) on PKC-mediated germinal
20 vesicle breakdown (GVBD) in the absence of insulin induction.

Figure 5C shows the effects of injecting peptide rIII (SEQ ID NO:4) on PKC-mediated germinal vesicle breakdown (GVBD) in the absence of insulin induction.

Figure 6 shows the distribution of β PKC in *Xenopus*
25 oocytes between the cytosolic and membrane-associated fractions following microinjection of either injection solution, peptide I (SEQ ID NO:1) or peptide rVI (SEQ ID NO:7) with or without insulin stimulation.

Figure 7 shows the effects of peptides I and rVI on
30 the sensitivity of β PKC to Arg-C endopeptidase.

Figure 8 shows the effects of peptides I and rVI on PKC autophosphorylation in the absence of PKC activators.

Figure 9 shows the effects of peptides I and rVI on PKC phosphorylation of histones in the absence of PKC
35 activators.

Figure 10 shows the effects of peptide rIII on PKC phosphorylation of histones in the absence of PKC activators.

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Figure 11 shows the amino acid sequence of the 56 kDa human protein with the WD-40 repeats aligned and putative binding peptide regions delineated by a box.

Figure 12 shows the amino acid sequence of the AAC-rich protein with the WD-40 repeats aligned and putative binding peptide regions delineated by a box.

Figure 13 shows the amino acid sequence of the B-TRCP protein with the WD-40 repeats aligned and putative binding peptide regions delineated by a box.

Figure 14 shows the amino acid sequence of the Beta-prime-COP protein with the WD-40 repeats aligned and putative binding peptide regions delineated by a box.

Figure 15 shows the amino acid sequence of the CDC4 protein with the WD-40 repeats aligned and putative binding peptide regions delineated by a box.

Figure 16 shows the amino acid sequence of the Chlam-3 protein with the WD-40 repeats aligned and putative binding peptide regions delineated by a box.

Figure 17 shows the amino acid sequence of the COP-1 protein with the WD-40 repeats aligned and putative binding peptide regions delineated by a box.

Figure 18 shows the amino acid sequence of the CORO protein with the WD-40 repeats aligned and putative binding peptide regions delineated by a box.

Figure 19 shows the amino acid sequence of the Coronin p55 protein with the WD-40 repeats aligned and putative binding peptide regions delineated by a box.

Figure 20 shows the amino acid sequence of the Cstf 50 kDa protein with the WD-40 repeats aligned and putative binding peptide regions delineated by a box.

Figure 21 shows the amino acid sequence of the bovine G-beta-1 protein with the WD-40 repeats aligned and putative binding peptide regions delineated by a box.

Figure 22 shows the amino acid sequence of the bovine G-beta-2 protein with the WD-40 repeats aligned and putative binding peptide regions delineated by a box.

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Figure 23 shows the amino acid sequence of the drosophila G-beta protein with the WD-40 repeats aligned and putative binding peptide regions delineated by a box.

Figure 24 shows the amino acid sequence of the human G-beta-1 protein with the WD-40 repeats aligned and putative binding peptide regions delineated by a box.

Figure 25 shows the amino acid sequence of the human G-beta-2 protein with the WD-40 repeats aligned and putative binding peptide regions delineated by a box.

Figure 26 shows the amino acid sequence of the mouse G-beta protein with the WD-40 repeats aligned and putative binding peptide regions delineated by a box.

Figure 27 shows the amino acid sequence of the drosophila groucho protein with the WD-40 repeats aligned and putative binding peptide regions delineated by a box.

Figure 28 shows the amino acid sequence of the squid GTP-binding protein with the WD-40 repeats aligned and putative binding peptide regions delineated by a box.

Figure 29 shows the amino acid sequence of the HSIEF 930 protein with the WD-40 repeats aligned and putative binding peptide regions delineated by a box.

Figure 30 shows the amino acid sequence of the human 12.3 protein with the WD-40 repeats aligned and putative binding peptide regions delineated by a box.

Figure 31 shows the amino acid sequence of the human IEF-7442 protein with the WD-40 repeats aligned and putative binding peptide regions delineated by a box.

Figure 32 shows the amino acid sequence of the insulin-like growth factor binding protein complex with the WD-40 repeats aligned and putative binding peptide regions delineated by a box.

Figure 33 shows the amino acid sequence of the rat insulin-like growth factor binding protein with the WD-40 repeats aligned and putative binding peptide regions delineated by a box.

Figure 34 shows the amino acid sequence of the human LIS1 protein with the WD-40 repeats aligned and putative binding peptide regions delineated by a box.

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Figure 35 shows the amino acid sequence of the MD6 protein with the WD-40 repeats aligned and putative binding peptide regions delineated by a box.

Figure 36 shows the amino acid sequence of the yeast
5 MSI1 protein with the WD-40 repeats aligned and putative binding peptide regions delineated by a box.

Figure 37 shows the amino acid sequence of the mouse pc326 MUS protein with the WD-40 repeats aligned and putative binding peptide regions delineated by a box.

10 Figure 38 shows the amino acid sequence of the ORD RB1 protein with the WD-40 repeats aligned and putative binding peptide regions delineated by a box.

Figure 39 shows the amino acid sequence of the periodic trp protein with the WD-40 repeats aligned and putative
15 binding peptide regions delineated by a box.

Figure 40 shows the amino acid sequence of the PLAP protein with the WD-40 repeats aligned and putative binding peptide regions delineated by a box.

Figure 41 shows the amino acid sequence of the
20 retinoblastoma binding protein with the WD-40 repeats aligned and putative binding peptide regions delineated by a box.

Figure 42 shows the amino acid sequence of the S253 protein with the WD-40 repeats aligned and putative binding peptide regions delineated by a box.

25 Figure 43 shows the amino acid sequence of the SOF1 protein with the WD-40 repeats aligned and putative binding peptide regions delineated by a box.

Figure 44 shows the amino acid sequence of the STE4 yeast protein with the WD-40 repeats aligned and putative
30 binding peptide regions delineated by a box.

Figure 45 shows the amino acid sequence of the TF1 transcription factor protein with the WD-40 repeats aligned and putative binding peptide regions delineated by a box.

Figure 46 shows the amino acid sequence of the TUP1
35 protein with the WD-40 repeats aligned and putative binding peptide regions delineated by a box.

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Figure 47 shows the amino acid sequence of the TUP1 homolog protein with the WD-40 repeats aligned and putative binding peptide regions delineated by a box.

Figure 48 shows the amino acid sequence of the YCU7 protein with the WD-40 repeats aligned and putative binding peptide regions delineated by a box.

Figure 49 shows the amino acid sequence of the YCW2 protein with the WD-40 repeats aligned and putative binding peptide regions delineated by a box.

Figure 50 shows the amino acid sequence of the YKL25 protein with the WD-40 repeats aligned and putative binding peptide regions delineated by a box.

Figure 51 shows the amino acid sequence of the YRB140 protein with the WD-40 repeats aligned and putative binding peptide regions delineated by a box.

Detailed Description of the Invention

I. Definitions

Unless otherwise indicated, all terms used herein have the same meaning as they would to one skilled in the art of the present invention. Practitioners are particularly directed to Current Protocols in Molecular Biology (Ausubel) for definitions and terms of the art.

Abbreviations for amino acid residues are the standard 3-letter and/or 1-letter codes used in the art to refer to one of the 20 common L-amino acids. Likewise, abbreviations for nucleic acids are the standard codes used in the art.

An "amino acid group" refers to a group of amino acids where the group is based on common properties, such as hydrophobicity, charge, or size.

A "conserved set" of amino acids refers to a contiguous sequence of amino acids that is conserved between members of a group of proteins. A conserved set may be anywhere from two to over 50 amino acid residues in length. Typically, a conserved set is between two and ten contiguous residues in length. The individual positions within a conserved set each typically comprise one of several amino acids, selected from an amino acid group(s). In cases where a residue is 100% conserved

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at a particular position, the conserved set sequence will contain only that residue at that position. For example, for the two peptides WRTAA (SEQ ID NO:263) and WRTAV (SEQ ID NO:264), there are 4 identical positions (WRTA; SEQ ID NO:265) and one position where the residue is an "A" or a "V".

Proteins are typically long chains of amino acid based polyamides (polypeptides) capable of creating secondary and tertiary structure. Proteins may be composed of one, two or more polypeptide chains and may further contain some other type of substance in association with the polypeptide chain(s), such as metal ions or carbohydrates. The size of proteins covers a rather wide range from ~5,000 to several hundred thousand g/mole. The 5,000 figure corresponds to the presence of roughly 40-45 amino acids.

Unless otherwise indicated, the sequence for proteins and peptides is given in the order from the amino terminus to the carboxyl terminus. Similarly, the sequence for nucleic acids is given in the order from the 5' end to the 3' end.

The term "interacting proteins" refers to a pair of polypeptides that can form a stably-associated complex due to, for example, electrostatic, hydrophobic, ionic and/or hydrogen-bond interactions under physiological conditions.

Proteins smaller than about 5,000 g/mole are typically referred to as polypeptides or simply peptides (Bohinski).

Two amino acid sequences or two nucleotide sequences are considered homologous (as this term is preferably used in this specification) if they have an alignment score of >5 (in standard deviation units) using the program ALIGN with the mutation gap matrix and a gap penalty of 6 or greater (Dayhoff). The two sequences (or parts thereof) are more preferably homologous if their amino acids are greater than or equal to 50%, more preferably 70%, still more preferably 80%, identical when optimally aligned using the ALIGN program mentioned above.

A peptide or peptide fragment is "derived from" a parent peptide or polypeptide if it has an amino acid sequence that is identical or homologous to the amino acid sequence of the parent peptide or polypeptide. Homologous peptides are defined above. Exemplary derived peptides are peptide rIII (SEQ

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ID NO:4) and peptide rVI (SEQ ID NO:7), which are derived from the third and seventh WD-40 repeats of RACK1 (SEQ ID NO:27), respectively.

The term "expression vector" refers to vectors that have the ability to incorporate and express heterologous DNA fragments in a foreign cell. Many prokaryotic and eukaryotic expression vectors are commercially available. Selection of appropriate expression vectors is within the knowledge of those having skill in the art.

The term "PKC" refers to protein kinase C, or C-kinase.

The term "RACK" refers to receptor for activated C-kinase.

The term "PS" refers to phosphatidylserine.

The term "DG" refers to diacylglycerol.

The term "PL" refers to phospholipids. Phospholipids include both phosphatidylserine and diacylglycerol.

The term "GVBD" refers to germinal vesicle breakdown, a measure of insulin-induced maturation in *Xenopus* oocytes.

The term "PCR" refers to polymerase chain reaction.

The term "NMR" refers to nuclear magnetic resonance.

The term " β ARK" refers to β -adrenergic receptor kinase.

II. General Overview of Invention.

The invention relates to interacting proteins, at least one of which contains an amino acid sequence with one or more of the characteristic repeats termed WD-40 (Fong, et al.).

According to one aspect of the invention, the function of a first protein of a pair of interacting proteins may be modulated, altered or disrupted by the addition, to a solution or medium containing the protein, of a peptide having a sequence that is identical or homologous to a part of the sequence of a WD-40 motif-containing repeat present in a second protein of the pair of interacting proteins.

The modulation or disruption of function of the first protein is due to the binding or association of the WD-40-derived peptide, termed "binding peptide", with the first

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protein. The consequences of the binding or association of the binding peptide with the first protein depend on the sequence of the peptide.

Typically, the presence of the binding peptide will inhibit the binding of the first protein to the second protein. This binding may be assayed *in vitro* by, for example, an overlay assay, whereby the degree of binding of one protein to another may be assessed. Several adaptations of overlay assays applied to embodiments of the present invention are described herein.

Regardless of whether or not the WD-40-derived peptide affects the association of the first protein with the second protein, the peptide may alter or modulate defined activities of the first protein. These activities may be assayed by a variety of methods *in vivo* and/or *in vitro*. The method(s) employed depend on the protein whose activity is being measured.

An exemplary first protein of a pair of interacting proteins is protein kinase C (PKC). Upon activation, PKC interacts with receptors for activated C kinase (RACKs), at least one of which (RACK1) contains WD-40 repeats. Several assays for determining the activity of PKC in the presence and in the absence of peptides derived from the WD-40 region of RACK1 are detailed herein.

Certain "interacting proteins" interact only after one or more of them has been stimulated by an exogenous or endogenous factor(s). For instance, PKC, as shown herein, does not bind to RACK proteins until it has been activated by, for example, phosphatidylserine (PS), diacylglycerol (DG) and calcium. However, peptides derived from WD-40 repeats of a second protein of such a pair may be able to associate with or bind to the first protein even in the absence of activators of the first protein, and in so doing, affect the function of the first protein (e.g. activate, inactivate, potentiate, sensitize, desensitize, alter the specificity, etc.).

Binding peptides derived from WD-40 repeats of a second protein of a pair of interacting proteins, may be useful as specific agonists, antagonists, potentiators of function, and the like, of the first protein of the pair. These properties may make the peptides useful in a number of applications, for

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example, direct use in therapeutic applications or as lead compounds for the development of other therapeutic agents, e.g., small organic molecules.

III. Advantages of the Invention for the Inhibition of Activated PKC Binding to RACK1.

Protein kinase C (PKC) is a family of at least 10 isozymes that share common structures and biochemical characteristics. It has been demonstrated that several isozymes are present within a single cell type, and it has been assumed that individual PKC isozymes are involved in different cellular functions. However, so far, the available activators and inhibitors of PKC do not appear to be isozyme-specific. Therefore, it is currently impossible to determine the role of individual PKC isozymes in normal cellular functions as well as in disease.

PKC activation by, for example, diacylglycerol and calcium, induces the translocation of PKC from a soluble (cytosolic) to a cell particulate (membrane-associated) fraction, as shown in experiments herein (Example 8). Activated PKC is stabilized in the cell particulate fraction by binding to membrane-associated receptors (receptors for activated C-Kinase, or RACKs).

In experiments done in support of the present invention and described herein, a clone (pRACK1) encoding a RACK has been isolated (Example 1). RACK1 belongs to a growing family of proteins that are homologous to the β -subunit of transducin and contain the WD-40 motif (Fong, et al.). It was demonstrated that peptide I (SEQ ID NO:1) binds to purified PKC (see Example 6 and Fig. 4); inhibits the binding of PKC to purified recombinant RACK1 protein (see Example 4 and Fig. 3), and inhibits PKC activity in several in vivo and in vitro assays (see Examples 7-11 and Figs. 5-9).

Peptide I (SEQ ID NO:1) is homologous to a sequence identified in the sixth WD-40 repeats of RACK1 (see Fig. 1C). A synthetic peptide was prepared based on this sequence (peptide rVI; SEQ ID NO:7; underlined amino acids in repeat VI of Fig. 1C). Six more peptides were also prepared based on the

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corresponding regions in repeats I-V and VII (peptides rI-rV, rVII; SEQ ID NO:2-6, 8; underlined regions in corresponding repeats, Fig. 1C). Some of the peptides were also found to inhibit the binding of PKC to RACK1 (see Example 4 and Fig. 3).

5 In addition, some of the peptides were found to bind to purified PKC (see Example 6, Fig. 4), partially activate PKC in the absence of other activators (peptide rVI; see Examples 7, 10, 11 and Figs. 5, 8 and 9), and potentiate the effects of known PKC activators on the enzyme (see Examples 7-9 and Figs. 5-7).

10 In *Xenopus* oocyte maturation studies (see, for instance, Example 7), peptide rVI (SEQ ID NO:7) is an agonist of β PKC. Peptide rIII, while less potent, is also an agonist of PKC; it enhances insulin-induced oocyte maturation at 50 and 500 μ M.

15 In cardiac myocytes, norepinephrine (NE, 2 μ M) causes translocation of δ and ϵ PKC isozymes from the cytosolic to the particulate fraction. Introduction into cardiac myocytes of peptide rIII, and to a lesser extent peptide rVI, caused an immediate translocation of δ and ϵ PKC isozymes in the absence of
20 hormone stimulation. This peptide-induced translocation was followed by degradation of δ and ϵ PKC isozymes. Moreover, NE-induced translocation is further enhanced in cells containing peptide rIII.

In contrast, introduction of peptide I to these cells does
25 not affect PKC distribution in the absence of hormone stimulation, nor does it induce PKC degradation. Furthermore, NE-induced translocation is inhibited by peptide I. Similar concentrations of a number of control peptides did not affect PKC distribution or degradation in control or NE-treated cells.

30 In studies on rat cardiac myocytes, peptide rIII induced δ PKC and ϵ PKC activation that was followed by degradation of these activated isozymes.

Peptide rVI also augments hormone-induced translocation of PKC isozymes (see, for example, Example 8 and
35 Fig. 6). In contrast, peptide I (SEQ ID NO:1) inhibited hormone-induced translocation of PKC isozymes (Example 8, Fig 6) and did not cause degradation.

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The data summarized above demonstrate that peptides derived from WD-40 repeats of RACK1 can serve as PKC agonists and antagonists *in vivo*, and suggest that peptides derived from WD-40 regions of RACK1 contain at least part of the protein-protein interface between PKC and RACK1.

Furthermore, the results suggest that (i) WD-40 repeats present in other proteins, such as G β subunit, may also be located at or near a surface involved in protein-protein interactions, (ii) peptides derived from these repeats may be effective in disrupting the interactions of the proteins with their partners (e.g. β -adrenergic receptor kinase (β ARK)), (iii) the peptides may modulate or alter the activity of the proteins with which the WD-40 repeat-containing proteins interact, and (iv) the peptides may therefore have specific biological effects when administered *in vivo*.

IV. Identification of Pairs of Interacting Proteins.

A. Biochemical Approaches.

Novel interacting proteins may be identified and isolated by a number of methods known to those skilled in the art. For example, monoclonal antibodies raised to a mixture of antigens, such as a particular tissue homogenate, may be characterized and used to immunoprecipitate a single class of antigen molecules present in that tissue. The precipitated proteins may then be characterized further, and used to co-precipitate other proteins with which they normally interact (Hari, et al., Escobedo, et al.).

An alternate method to identify unknown polypeptides that interact with a known, isolated protein is by the use of, for example, an overlay assay (Wolf, et al., Mochly-Rosen, et al., 1991). A mixture (such as a fraction of a tissue homogenate, for example, a Triton-insoluble protein fraction) potentially containing proteins that bind to a known, isolated protein can be resolved using PAGE, blotted onto a nitrocellulose or nylon membrane, and contacted with a solution containing the known protein and any necessary co-factors or small molecules. After washing, the membrane can be contacted

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with a probe for the known protein, for example an antibody or a mixture of antibodies, and the signal visualized.

B. Molecular Approaches.

Putative binding proteins of a known protein may be isolated from tissue homogenates, as described above. Alternatively, DNA clones encoding putative binding proteins may be identified by screening, for example, an appropriate cDNA expression library. Expression libraries made from a wide variety of tissues are commercially available (for example, from Clonetech, Palo Alto, CA). Expression libraries may also be made *de novo* from organisms and tissues of choice by practitioners skilled in the art.

The screening of expression libraries for clones expressing a protein or protein fragment of interest may be readily accomplished using techniques known in the art, for example, an overlay assay.

An overlay-assay screening method may be used to identify clones expressing a (known or unknown) protein or protein fragment that binds to a probe in hand. The probe may be a protein postulated to be involved in protein-protein interactions with a protein expected to be present in a cDNA library selected for screening (as was the case for the cloning of RACK1, detailed in Example 1).

Actual screening of a selected cDNA library may be accomplished by inducing plated clones to express cloned exogenous sequences, transferring replicas of the induced plaques or colonies to filter membranes, and screening the membranes with an appropriate probe. According to this method, lifts of filters (for example, nylon or nitrocellulose) from an appropriately-induced cDNA library plates (induced by, for example, IPTG) are washed, blocked, and incubated with a selected probe for a period of time sufficient to allow the selected probe(s) to bind specifically to polypeptide fragments present on the filters. The filters may then be washed and reacted with a reagent (for example, antibodies such as alkaline phosphatase-conjugated goat anti-rabbit or anti-mouse antibodies, available from Boehringer Mannheim Biochemicals,

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Indianapolis, IN). Additional reactions may be carried out as required to detect the presence of bound probe.

One such overlay assay, described in Example 1, was used to screen a rat brain cDNA expression library for proteins that bind purified PKC in the presence of PKC activators (phosphatidylserine, diacylglycerol and calcium). The filters were screened with a mixture of rat brain PKC isozymes (α , β , γ , δ , ϵ and ζ). Following a series of washes, bound PKC isozymes were detected with a mixture of anti- α , β , γ PKC mouse monoclonal antibodies, and anti- δ , ϵ and ζ PKC rabbit polyclonal antibodies. Bound antibodies were detected using alkaline phosphatase-conjugated goat anti-rabbit or anti-mouse antibodies and 5-bromo-4-chloro-3-indoyl phosphate p-toluidine salt as a substrate.

Once a clone is identified in a screen such as the one described above, it can be isolated or plaque purified and sequenced. The insert may then be used in other cloning reactions, for example, cloning into an expression vector that enables efficient production of recombinant fusion protein. Examples of appropriate expression vectors are pGEX (Smith, et al., 1988) and pMAL-c2 (New England BioLabs, Beverly, MA). An expression vector containing an insert of interest may be used to transform appropriate host cells, such as *E. coli*, and the transformed host cells can be used to produce the recombinant protein in large amounts.

Typically, a recombinant protein is expressed in tandem with a bacterial or viral gene product (endogenous polypeptide) as part of a fusion protein. The junction between the endogenous polypeptide and the recombinant protein typically includes a recognition site for a rare-cutting protease. The endogenous peptide may be designed to incorporate a unique affinity tag (a short peptide sequence) to facilitate the purification of the fusion protein with an affinity reagent, such an antibody directed against the affinity tag. The recombinant protein may then be purified from the fusion protein using the appropriate protease.

Purified recombinant protein may be used in a number of ways, including in an overlay binding assay to screen for

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peptides or substances that inhibit binding between the recombinant protein and an interacting protein.

An example of the use of a cDNA clone to express protein is detailed in Example 2. RACK1 cDNA, isolated as described above and in Example 1, was subcloned into an expression vector (pMAL-c2, New England BioLabs, Beverly, MA) capable of expressing a cloned insert in tandem with maltose-binding protein (MBP). The vector containing the RACK1 insert was used to transform TB1 *E. coli*, which were then induced with IPTG. The cells produced a 78 kDa fusion protein comprised of RACK1 fused to the MBP. The overexpressed fusion protein was purified on an amylose affinity column according to the manufacture's protocol (New England BioLabs, Beverly, MA) and incubated with protease Xa to separate the expressed insert from the MBP. Following the incubation, a 36 kDa RACK1 protein was obtained.

V. Identification of WD-40 Repeats.

According to a method of the present invention, protein-protein interactions can be disrupted and/or the activity of an interacting protein can be altered, given at least one of the interacting proteins contains a WD-40 motif, or region, with a peptide(s) derived from a WD-40 repeat(s) of one of the proteins.

WD-40 repeats are typically found in a family of proteins having at least a limited homology with the β subunit of transducin. WD-40 repeats present in a selected member of this family can be identified by (A) performing a self-homology analysis on a selected protein using a homology matrix (performed by, for example, the computer program DNA Strider 1.2, available from Christian Marck, Service de Biochimie et de Genetique Moleculaire, Department de Biologie Cellulaire et Moleculaire, Direction des Sciences de la Vie - CEA - FRANCE), (B) aligning sequences comprising the repeating elements revealed by the homology matrix analysis, and (C) identifying conserved amino acid residues that typically serve to define a WD-40 repeat. The steps are discussed individually, below.

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A. Homology matrix analysis.

Determining whether a particular amino acid sequence contains repeated motifs may be accomplished by a number of methods known to those skilled in the art. They range from a simple visual inspection of the sequence to the use of computer programs which can identify repeated motifs. One widely-implemented computer-assisted method is to generate a self-homology matrix. A self-homology matrix computes the homology of each amino acid residue in a particular sequence with every other residue in that sequence. The homology scores are stored in a 2-dimensional matrix.

Values higher than a selected criterion level are flagged and displayed as points on an x-y coordinate. The x- and y-axes correspond to consecutive amino acid positions in the sequence.

An example of a self-homology matrix analysis is shown in Figure 1B. The matrix was generated using the computer program DNA Strider 1.2 (Christian Marck, Service de Biochimie et de Genetique Moleculaire, Department de Biologie Cellulaire et Moleculaire, Direction des Sciences de la Vie - CEA - FRANCE) with the amino acid sequence of RACK1 (SEQ ID NO:27) with a window setting of 21 and a stringency of 6. Some typical features of a self-homology matrix are evident in the figure. The graph shows a "primary" diagonal line extending from the origin with a slope of unity, corresponding to the fact that the sequence is identical to itself. If the sequence contains repeating elements, as RACK1 does, there will be other, shorter sets of contiguous points arranged in diagonal lines substantially parallel to the primary diagonal and offset from the primary diagonal in the x- or y-directions. These shorter lines identify the locations of repeating elements with the sequence. Each repeating element will result in two sets of displayed points, symmetrically distributed about the primary diagonal.

The data displayed in a homology matrix analysis can be used to locate and roughly align the sequences of repeating elements for a more detailed analysis. The horizontal band delineating the region between ~100 and ~130 on the y-axis in

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Fig. 1B highlights the fact that portions of that region of RACK1, that is, the amino acids between about amino acid 100 and amino acid 130, are repeated a total of seven times in the sequence of RACK1. Arrows point to the repeats in the homology matrix. For purposes of rough alignment, the short diagonal lines pointed out by the arrows can be extended to the horizontal line at amino acid ~100 on the y-axis, and the x-axis location corresponding to the intersection be noted. For example, the intersection corresponding to the second repeat (second arrow from the left) is at $x \sim 50$).

Values determined in this manner may then be used to align the amino acid sequence of the repeats with each consecutive repeat beneath the preceding one, the start of each repeat corresponding approximately to the amino acid position determined by the analysis in the preceding paragraph. The amino acid sequence of RACK1, aligned in this manner, is shown in Fig. 1C.

Most commercially-available DNA and protein sequence analysis programs have the capability to perform a self-homology matrix analysis. One example is the program DNA Strider 1.2 (Christian Marck, Service de Biochimie et de Genetique Moleculaire, Department de Biologie Cellulaire et Moleculaire, Direction des Sciences de la Vie - CEA - FRANCE).

Once the repeating elements are identified and the sequences corresponding to repeating elements are roughly aligned, one may proceed to define the degree of homology among the individual repeats at the specific positions within the repeats, as is described below.

B. Aligning amino acid sequences.

If a self-homology matrix was used to obtain a crude alignment, the sequences may aligned by eye on a personal computer or the like using, for example, a text editor, a drawing program or a sequence-analysis program. Examples of programs effective to accomplish an alignment include "MACDRAW PRO" (Claris Corp., Santa Clara, CA) and "WORD" (Microsoft Corp., Redmond, WA), both of which are available for "MACINTOSH" series computers (Apple Computer Corporation, Cupertino, CA), as

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well as IBM-compatible computers running "WINDOWS" (Microsoft Corp.).

Amino acid sequences corresponding to internal repeats can also be aligned automatically using a protein sequence analysis program, such as "MACVECTOR" (Eastman Kodak Co., New Haven, CT).

According to a method of the invention, aligned sequences are examined further to determine if they fulfil criteria to be defined as WD-40 repeats. These criteria are detailed in part C, below.

C. Amino acid residues that define a WD-40 repeat.

Upon completion of steps outlined in parts A and B above, that is, determining whether a particular protein contains internal repeats, and if so, aligning those repeats, it is necessary to determine whether the aligned repeats contain WD-40 regions.

A WD-40 motif is roughly defined as a contiguous sequence of about 25 to 50 amino acids with relatively-well conserved sets of amino acids at the two ends (amino- and carboxyl-terminal) of the sequence. Conserved sets of at least one WD-40 repeat of a WD-40 repeat-containing protein typically contain conserved amino acids at certain positions. The amino-terminal set, comprised of two contiguous amino acids, often contains a Gly followed by a His. The carboxyl-terminal set, comprised of six to eight contiguous amino acids, typically contains an Asp at its first position, and a Trp followed by an Asp at its last two positions.

A more accurate definition of a WD-40 motif incorporates the observation that while specific residues, such as those identified above, are not always conserved within a WD-40 motif, conserved positions within the motif are typically occupied by residues selected from a restricted class of amino acids.

In order to better define the class of conserved residues at selected positions, it is necessary to group amino acids on the basis of certain common properties. A functional way to define common properties between individual amino acids

is to analyze the normalized frequencies of amino acid changes between corresponding proteins of homologous organisms (Schulz). According to such analyses, groups of amino acids may be defined where amino acids within a group exchange preferentially with each other, and therefore resemble each other most in their impact on the overall protein structure (Schulz). Examples of amino acid groups defined in this manner, some of which are used in the definition of a WD-40 motif herein, include:

- (i) a charged group, consisting of Glu and Asp, Lys, Arg and His,
- (ii) a positively-charged group, consisting of Lys, Arg and His,
- (iii) a negatively-charged group, consisting of Glu and Asp,
- (iv) an aromatic group, consisting of Phe, Tyr and Trp,
- (v) a nitrogen ring group, consisting of His and Trp,
- (vi) a large aliphatic nonpolar group, consisting of Val, Leu and Ile,
- (vii) a slightly-polar group, consisting of Met and Cys,
- (viii) a small-residue group, consisting of Ser, Thr, Asp, Asn, Gly, Ala, Glu, Gln and Pro,
- (ix) an aliphatic group consisting of Val, Leu, Ile, Met and Cys, and
- (x) a small hydroxyl group consisting of Ser and Thr.

In addition to the groups presented above, each amino acid residue may form its own group, and the group formed by an individual amino acid may be referred to simply by the one and/or three letter abbreviation for that amino acid commonly used in the art.

A "WD-40" motif is defined herein as a contiguous set of amino acids between (inclusive) two sets of relatively well conserved residues, termed herein as an "amino-terminal set" and a "carboxyl-terminal set".

The amino-terminal set contains two adjacent amino acids. The residue at the first position is typically selected from groups ii, vi or viii, while the residue at the second position is typically selected from groups i, x or Ile. The first and second positions will often consist of Gly and His,

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respectively. The Gly and His residues are typically present in at least one of the aligned repeats of a WD-40-containing protein.

The carboxyl-terminal conserved set typically includes
5 eight residues, but may contain as few as six residues. The most well-conserved residue in WD-40 motifs identified thus far is an Asp residue, comprising the first amino acid of the carboxyl-terminal conserved set. It is present in virtually all WD-40 repeats illustrated herein. In those repeats where it is
10 not present, the position is occupied by a residue from groups iii or Gly.

The last two amino acids in the carboxyl-terminal conserved set are typically selected from groups iv or Ile, and groups i or viii, respectively. The most commonly used residue
15 at the first of these positions is Trp. It is typically present in at least one of the WD-40 repeats of any given protein. The second position is occupied less consistently by a single residue, but is often occupied by Asp. The Trp-Asp (WD) combination is part of the namesake of WD-40 repeats.

20 The amino acids present in the internal portion of the carboxyl-terminal conserved set are less well-conserved than the terminal residues, and their total number may differ by up to two residues in different WD-40 repeats. The third position in from the carboxyl-terminal end of the carboxyl-terminal
25 conserved set is typically selected from groups viii or ix, more typically ix. The fifth position in from the carboxyl-terminal end of the carboxyl-terminal conserved set is also typically selected from groups viii or ix, more typically ix.

The length of a WD-40 repeat, including the amino-
30 terminal and carboxyl-terminal conserved sets is typically between about 25 and about 50 residues, more typically between about 29 and 34 residues. The distribution arises primarily from differences in the number of residues present between the amino-terminal and carboxyl-terminal conserved sets.

35 The number of WD-40 repeats in a particular protein can range from two to more than eight. The average number is about 5.

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A determination of whether or not a set of aligned internal repeats are WD-40 repeats can be facilitated by an examination of all of the repeats as a whole, rather than an examination of each repeat individually. This is in part
5 because not all of the aligned repeats will necessarily contain all of the conserved sequences that serve to identify WD-40 repeats, although the conserved residues will typically appear in at least one of the repeats.

For example, Fig. 1C shows the RACK1 amino acid
10 sequence aligned to illustrate the internal repeats present in the sequence. All of the repeats are WD-40 repeats, even though the amino-terminal conserved set of repeat VI, for instance, contains an "LD" as opposed to the more usual "GH", and the carboxyl-terminal conserved set contains a "G" at its first
15 position, as opposed to the highly-conserved "D". Similarly, the carboxyl-conserved set of, for example, repeat I, contains a "WK" at the last to positions, as opposed to the more usual "WD".

It will be appreciated that certain residues or sets
20 of residues will be well-conserved in the WD-40 repeats of a selected protein, even though they may not be conserved in WD-40 repeats in general. Such residues or sets of residues may be useful in several ways. For example, they may be used in performing an alignment of internal repeats in a selected
25 protein, as described in part B, above. The residues may also be useful for identifying regions based on which effective binding peptides may be designed (see section VI., below).

D. Identification of WD-40 repeats in RACK1.

In experiments done in support of the present
30 invention, a protein that binds to activated PKC was cloned and sequenced (see Example 1). Sequence analysis of the deduced amino acid sequence revealed the presence of repeats, which were aligned and are shown in Figure 1C.

The aligned repeats were identified as WD-40 repeats
35 by application of the criteria identified in parts A, B and C above. For example, the conserved amino-terminal set in repeats I, II, III and V consists of the typical "GH", whereas in

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repeats IV, VI and VII, the set consists of other residues. These other residues, however, are contained in at least one of the amino acid groups identified above as conserved at the appropriate position. The conserved carboxyl-terminal set
5 contains the highly-conserved "D" at its first position in all repeats except repeat VI. The second-to-last position of this set contains the relatively-well conserved "W" in each repeat, while the last position contains the typical "D" in repeats II, V and VI, and other residues in the other repeats.

10 Taken together, these data indicate that the repeats contained in RACK1 are WD-40 repeats. The data also illustrate that not all repeats contain all of the elements typical of a WD-40 motif, but that when the repeats are aligned and viewed together as a whole, a WD-40 motif is apparent in all repeats.

15 E. Identification of WD-40 repeats in sequenced proteins.

Data were compiled in support of the present invention to illustrate how WD-40 repeats in various proteins may be identified, and to illustrate the diversity of amino acid sequences that may be properly identified as WD-40 repeats by
20 those skilled in the art following the guidance set forth herein. Two methods that were used to identify WD-40-containing protein sequences are detailed in Example 7.

In the first method, proteins identified in their description as having a homology to β -transducin were examined
25 as detailed in parts B-D, above, for WD-40 repeats. 30 proteins were identified in this manner. The amino acid sequences of these proteins, with the WD-40 regions aligned and delineated, are shown in Figs. 12-18, 20-27, 29-30, 34-35, 37-38, 40 and 42-50. The sequences are represented in the Sequence Listing as
30 SEQ ID NO:29-35, 37-44, 46-47, 51-52, 54-55, 57 and 59-67.

In the second method, proteins whose sequences were homologous to a consensus WD-40 motif (SEQ ID NO:262), were identified and examined for WD-40 repeats. Ten additional proteins containing WD-40 repeats were identified with this
35 strategy. The amino acid sequences of those proteins, with the WD-40 repeats aligned and delineated, are shown in Figs. 11, 19, 28, 31-33, 36, 39, 41 and 51. The sequences are represented in

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the Sequence Listing as SEQ ID NO:28, 36, 45, 48-50, 53, 56, 58, and 68.

Other types of searches may be equally effective at identifying proteins which may contain WD-40 repeats. For example, on-line databases such as GenBank or SwissProt can be searched, either with an entire sequence of a WD-40-containing protein, or with a consensus WD-40 repeat sequence. Various search algorithms and/or programs may be used, including FASTA, BLAST or ENTREZ. FASTA and BLAST are available as a part of the GCG sequence analysis package (University of Wisconsin, Madison, Wisconsin). ENTREZ is available through the National Center for Biotechnology Information, National Library of Medicine, National Institutes of Health, Bethesda, MD.

Sequences identified with a protein homology search are then analyzed as described in parts A, B and C, above, to identify potential WD-40 motifs. Once located, the motifs can be aligned, and effective binding peptides may be designed.

F. Identification of WD-40 regions in novel polypeptides.

WD-40 repeats may be identified in a novel polypeptide by, for example, the methods described in parts A-D above. It will be appreciated, however, that step A above (homology matrix) is not required in the identification of WD-40 repeats. Following the guidance of the present invention, one skilled in the art may, for instance, identify a WD-40 motif while scanning the sequence of some, perhaps novel, polypeptide merely through a recognition of one or more of the features characteristic of WD-40 repeats.

The precise methods by which one skilled in the art arrives at the conclusion that a particular motif is a WD-40 repeat is less relevant to the present invention than is the use of sequences derived from WD-40 motifs, regardless of how they are identified, to design peptides effective to alter or modulate the activity of one member of a pair of interacting proteins and/or to disrupt protein-protein interactions.

VI. Identification of Activity-altering Peptides.

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Upon the alignment and recognition of WD-40 repeats in a particular protein, one may proceed to design a peptide or a set of peptides that may be effective to associate with or bind to the protein with which the WD-40-containing protein normally associates. Such a binding or association may be expected to alter or modulate the activity of the protein and/or disrupt the association of the pair of interacting proteins.

The sequence of such a peptide will typically be homologous, if not identical to, a contiguous amino acid sequence contained within at least one of the WD-40 repeats. Examples of the selection of WD-40-derived peptides effective to disrupt protein-protein interactions are detailed in parts C and D below, for RACK-PKC and $G\beta/\gamma$ - β ARK interactions, respectively.

A. Choosing an appropriate region within a WD-40 repeat.

Putative binding peptides may be selected from any portion of a WD-40 repeat. If it is desired to obtain a degree of discrimination between the various WD-40-containing proteins, peptides should be chosen from the region between, and not including, the amino-terminal and carboxyl-terminal conserved sets. This "central region" typically shows greater sequence diversity between different WD-40-containing proteins than the terminal regions, and is roughly outlined by boxes in Figures 11-51, which show the amino acid sequences and aligned WD-40 repeats of various WD-40 repeat-containing proteins. Within the central region, peptides should be selected from sequences that have little or no homology to any other known sequences, save the sequence(s) of the protein(s) targeted for disruption.

For example, peptides rIII (SEQ ID NO:4, seven amino acids) and rVI (SEQ ID NO:7, eight amino acids), are identical to segments of RACK1 WD-40 repeats (III and VI, respectively) beginning five amino acids in from the amino termini of the WD-40 repeats from which they are derived (see Fig 1C, underlined segments). The WD-40 repeat segments corresponding to the binding peptides comprise the left portion of the central region of the respective WD-40 repeats, and are not well-conserved in RACK1.

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If it is desired to inhibit the interactions of, for example, all of the isoforms of a particular WD-40-containing protein family, a sequence is selected that includes a significant number of residues that are shared or highly homologous among at least one WD-40 repeat of each of the targeted isoforms.

If, on the other hand, an isoform-specific reagent is desired, a sequence is selected from a WD-40 repeat(s) of a specific isoform, where that sequence does not include a significant number of residues that are identical or highly homologous to residues in WD-40 sequences from related isoforms.

B. Choosing an appropriate length for a peptide.

Effective binding peptides may be designed that range in length from as few as about four residues to 40 or more residues. Preferably, binding peptides will have a length of at least about six residues, and less than about 20 residues. The length will be determined in part by the degree of desired homology to other WD-40 repeats, as described in part A above, and by the level of discrimination between proteins that is required.

For example, binding peptides selected from RACK1 sequences to inhibit RACK1/PKC interactions were seven and eight amino acids in length. The peptides are long enough to bind specifically to the targeted sequences, but short enough to not cross-react with other WD-40 repeat binding proteins. These properties enable the peptides to have very selective and specific effects, as is shown below in Examples 6-11.

C. Design of RACK1 WD-40-derived peptides to inhibit RACK1-PKC interactions.

Peptides rIII (SEQ ID NO:4, seven amino acids) and rVI (SEQ ID NO:7, eight amino acids) were designed in part following the guidance presented in parts A and B above. The peptides are identical to segments of RACK1 WD-40 repeat sequences beginning five amino acids in from the amino termini of the WD-40 repeats from which they are derived. The WD-40 repeat segments corresponding to the binding peptides comprise the left portion

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of the central region of the WD-40 repeats. The peptides were tested for their ability to disrupt protein-protein interactions *in vitro* and *in vivo*, as described in section VII and Examples 6-11 below.

5 D. Peptides derived from WD-40 repeats of Human G-Beta inhibit interactions of G-Beta subunits with β ARK.

Methods described in section V part E were used to identify WD-40 repeats (SEQ ID NO:128-134) in Human G-Beta (SEQ ID NO:41). Segments from the first six WD-40 repeats were
10 selected for the design of G-beta binding peptides (SEQ ID NO:13-18). The segments were selected based on criteria detailed in parts A and B, above.

The G-beta binding peptides are used to disrupt the interactions of G-beta subunits with β ARK. The disruption is
15 assayed using a modification of the overlay assay described in Example 4.

VII. Testing of Putative Binding Peptides.

Detailed below are several assays by which the efficacy of WD-40-derived peptides at binding to a target
20 protein, inhibiting protein-protein interactions, and altering or modulating the activity of a target protein may be determined.

One class of assays, widely-used to assess the binding of two proteins to each other, are overlay assays. Overlay
25 assays are generally applicable to most proteins. They can be used to, for example, assess the binding of WD-40-derived peptides to their targets, as shown in Example 6 and described in part B below. Overlay assays can also be used to assess the ability of WD-40-derived peptides to inhibit the binding of two
30 interacting proteins, one of which contains a WD-40 motif from which the peptides were derived (see, for instance, Example 4 and part C below).

Other assays may be used to assess effects of WD-40-derived peptides on the activity of the target protein. These
35 assays may be *in vivo* assays, *in vitro* assays, or a combination of *in vivo* and *in vitro* assays. The assay used will depend on

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the proteins involved and on the system(s) and/or process(es) that involve the interacting proteins against which the peptide was targeted. For instance, the assays described in parts D-I below are appropriate for characterizing PKC activity *in vivo* and *in vitro*.

While many of the assays below are particularly useful for characterizing the activity of PKC, they also illustrate a general framework of experiments by which the effects of WD-40 derived peptides on other proteins may be assessed.

A. Overlay assays to evaluate efficacy of putative binding peptides derived from WD-40 regions.

An overlay assay can be used to assess the disruption of the ability of a pair of proteins to associate. Methods for conducting overlay assays are well-known in the art (see, for example, Mochly-Rosen, et al., 1991).

Applications of overlay assays to evaluate putative binding peptides for PKC/RACK1 interactions are presented in Examples 4 and 5 herein. The assays can be generally described as follows.

One protein of a pair of interacting proteins ("immobilized" protein) can be resolved on an SDS/PAGE gel and blotted onto an appropriate membrane (for example, nitrocellulose or nylon) by methods known to those skilled in the art. The blots may then be contacted with a solution containing the other protein of the pair of interacting proteins ("overlay" protein) in the presence, and in the absence of putative binding peptides. Following appropriate wash steps, bound overlay protein can be detected by the use of an appropriate probe, such as an antibody directed against the overlay protein.

A variation on the above protocol may be performed to minimize a possible interference between unbound binding peptide and antibodies used to detect the presence of bound overlay protein. The modification consists of performing another SDS/PAGE electrophoresis between the steps of binding the overlay protein, and detecting the overlay protein with antibody or other probe. It is accomplished by cutting the blot into

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pieces sized to just encompass the area occupied by the blotted immobilized protein, after the overlay protein had been contacted (in the presence or in the absence of binding peptides) and allowed to bind to the blot. The pieces of membrane are then incubated in a sample buffer, placed in the wells of a second SDS polyacrylamide gel and subjected to electrophoresis.

Following electrophoresis, the gel is blotted as above, and contacted with a probe, for example antibodies, to detect bound overlay protein.

B. Binding of β PKC to peptides homologous to a WD-40 region of RACK1.

The binding of β PKC to peptide I (SEQ ID NO:1), peptide rVI (SEQ ID NO:7) and control peptide (SEQ ID NO:9) was assessed in Example 6 using a PKC overlay assay similar to that described in Example 3. Increasing amounts of peptides were applied onto nitrocellulose using a slot-blot apparatus. The membranes were incubated with PKC in the presence and absence of PS, DG, and calcium.

The data are shown in Figure 4, and show that activated PKC bound to both peptides I and rVI at peptide amounts as low as 5 μ moles, but not to the control peptide. Unactivated PKC did not bind to peptide I, but did bind to peptide rVI at similar concentrations.

The results indicate that while the peptides were homologous to one another and were capable of binding to the same protein, they behaved differently. Peptide rVI (SEQ ID NO:7; 8 residues) was able to bind to both activated as well as unactivated forms of PKC, whereas peptide I (SEQ ID NO:1; 15 residues) could bind only to activated PKC. The differences between the binding properties may be due, for example, to charge differences and/or length differences between the two peptides.

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C. Effects of peptides homologous to WD-40 region of RACK1 on PKC binding to RACK1

Two peptides (peptide rIII; SEQ ID NO:4 and peptide rVI; SEQ ID NO:7) identical to regions of RACK1 WD-40 repeats (underlined, Figure 1C) were tested for their ability to inhibit PKC binding to recombinant RACK1 using a modification of the overlay procedure referred to above. The experiment is detailed in Example 4 and the results are shown in Figure 3.

Peptide I caused an $81 \pm 6\%$ inhibition of PKC binding to recombinant RACK1 as compared with binding in the absence of added peptide. Both peptides rIII and rVI inhibited the binding of PKC to RACK1. In addition, peptides rI and rII were also effective inhibitors of the interaction of PKC to RACK1. A lesser inhibitory effect was obtained with peptides rIV and rV and no inhibition was obtained with peptide rVII.

The difference in the peptide's ability to inhibit binding may reflect differences in the roles played by the corresponding WD-40 repeats in the protein-protein interactions between PKC and RACK1. The peptide's ability or inability to inhibit protein-protein interactions as assayed by an overlay assay, however, is not necessarily correlated with the effects those peptides may have on the activity of the targeted proteins, as measured by both *in vivo* and *in vitro* assays and described in parts D-I below.

D. Effects of peptides homologous to WD-40 regions of RACK1 on PKC-mediated oocyte maturation.

Peptides I (SEQ ID NO:1), rIII (SEQ ID NO:4) and rVI (SEQ ID NO:7) were also tested for their ability to affect insulin-induced, PKC-mediated maturation in *Xenopus* oocytes, as detailed in Example 7 and shown in Figures 5A and 5C.

PKC is involved in the maturation of *Xenopus* oocytes. Phorbol esters, which activate PKC, or microinjection of a constitutively active mutant of PKC induce the first stage of oocyte maturation in the absence of hormones. Exposure to insulin causes an increase in diacylglycerol levels and microinjection of activated PKC enhances insulin-induced maturation (Stith, et al.). Microinjection of purified RACK

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proteins causes a significant decrease in the rate of oocyte maturation (Smith, et al., 1992). The insulin-induced oocyte maturation assay therefore provides an effective *in vivo* assay for compounds that interfere with the function of PKC.

5 The maturation response was quantified by monitoring the appearance of a white spot in the animal hemisphere of the oocyte, indicating germinal vesicle breakdown (GVBD) and maturation. The indicated peptides were microinjected into *Xenopus* oocytes and the percent of oocytes with GVBD following
10 insulin exposure was plotted as a function of time in Figures 5A and C.

 Approximately 80-85% of sham-injected (control) oocytes exposed to insulin reach maturation, as compared with 45-50% of oocytes injected with peptide I. The rate of
15 maturation of those oocytes that did mature was similar in the two cases. In contrast the effects of peptide I, both peptides rIII and rVI potentiated the effects of insulin on oocyte maturation, both in terms of the rate of maturation, and in the total fraction of oocytes that mature during the experiment.
20 Injection of peptides rIII or rVI increases the fraction of maturing oocytes to essentially 100%. Furthermore, peptide rVI induced oocyte maturation in the absence of insulin stimulation (Fig. 5B).

 Together, the data above indicate that peptides
25 homologous to the WD-40 region of RACK1 can modulate the function of a protein with which RACK1 interacts (e.g. PKC), that the modulation can occur *in vivo*, and that it can have clear and profound physiological consequences. Furthermore, the results with peptide rVI suggest that under appropriate
30 circumstances, the peptide alone may act to activate PKC, in the absence of other activating substances.

E. Effects of peptides homologous to WD-40 regions of RACK1 on PKC translocation in *Xenopus* oocytes.

 Insulin causes the redistribution of β PKC, but not
35 other PKC isozymes, from a cytosolic form to a membrane-associated form, as evidenced by the relative levels of PKC in the soluble vs. the particulate fraction of oocyte homogenate.

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To assess the effects of RACK1 WD-40-derived peptides on insulin-induced PKC translocation, 50 nl of a 20 mM NaCl solution containing the indicated peptides were microinjected into *Xenopus* oocytes. The oocytes were then homogenized, and the relative amount of PKC in the soluble and particulate fractions was assayed. The protocol followed was a modification of a method described by Smith, et al (1992). The results are shown in Figure 6.

Peptide I (50 μ M) did not affect β PKC distribution in untreated oocytes, but inhibited insulin-induced β PKC translocation (Fig. 3, lanes 7,8). In contrast, peptide rVI (50 μ M) induced β PKC translocation in the absence of insulin treatment (Fig. 3, lanes 3,4). These results suggest that peptide I is an antagonist of hormone-induced PKC translocation, whereas peptide rVI is an agonist and an activator of PKC translocation. In light of the results presented in Example 7, the data also suggest that the inhibition of insulin-induced GVBD following microinjection of peptide I was due to an inhibition of β PKC translocation.

F. Effects of peptides homologous to WD-40 regions of RACK1 on sensitivity of β PKC to Arg-C endopeptidase.

Upon activation of PKC, a pseudosubstrate autoinhibitory sequence at the N-terminus of PKC dissociates from the catalytic site and renders the molecule sensitive to endopeptidase Arg-C (Orr, et al.). Exposure of activated β PKC to Arg-C results in a limited proteolysis, or "nicking" of the enzyme. The nicking typically generates a 78 kDa fragment and several small fragments. Continued exposure to Arg-C typically results in the disappearance of β PKC (Orr, et al.).

Since peptides rIII (SEQ ID NO:4) and rVI (SEQ ID NO:7) exhibited PKC agonist activities in other assays (see, for instance Examples 7 and 8), experiments were performed to determine whether the peptides were capable of activating PKC in a manner to make it susceptible to endopeptidase Arg-C. The experiments are detailed in Example 9 and the results are shown in Figure 7.

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In the presence of effective concentrations of PKC activators (0.8 $\mu\text{g/ml}$ DG, 50 $\mu\text{g/ml}$ PS and 1 mM CaCl_2), exposure of βPKC to Arg-C resulted in nicking, generating the 78 kDa fragment (Fig. 7, lane 2). In the absence of PKC activators, exposure of βPKC (80 kDa) to endopeptidase Arg-C had no effect on the enzyme (Fig 7, lane 1).

Incubation of βPKC with Arg-C at low concentrations of activators (2.5 $\mu\text{g/ml}$ PS and 50 μM CaCl_2) in the absence of added peptide, in the presence of control peptide (SEQ ID NO:9) and in the presence of peptide I (SEQ ID NO:1) did not result in appreciable nicking activity (Fig. 7, lanes 4, 8 and 9, respectively). However, incubation of βPKC with the same low concentration of activators in the presence of peptides rIII or rVI resulted in the appearance of the 78 kDa nicked PKC fragment (effects of peptide rVI in Fig. 4, lanes 5-7). Concentrations as low as 10 nM of peptide rVI were sufficient to result in nicking activity, indicative of βPKC activation.

The results indicate that peptides rIII and rVI, but not peptide I, are effective to stabilize PKC in an activated conformation that renders it susceptible to Arg-C under conditions of low PKC activators that would otherwise not render the enzyme susceptible to Arg-C.

G. Effects of peptides homologous to WD-40 regions of RACK1 on βPKC autophosphorylation.

Activated PKC is capable of autophosphorylation, which can be assayed by incubation with [γ - ^{32}P]ATP and visualized on an autoradiograph of a gel. Anti-pseudosubstrate antibodies were shown previously to induce autophosphorylation in the absence of PKC activators (Makowske, et al.). Since peptide rVI (SEQ ID NO:7) was effective to induce PKC translocation and GVBD in the absence of PKC activators, experiments were performed to determine if the peptide was also capable of inducing PKC autophosphorylation. The experiments are detailed in Example 10 and the data are shown in Figure 8.

PKC activated with PS (50 $\mu\text{g/ml}$), DG (0.8 $\mu\text{g/ml}$) and CaCl_2 (1 mM) shows normal levels of autophosphorylation (lane 1). No autophosphorylation was seen in the absence of PKC activators

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(lane 2), or in the absence of PKC activators with peptide I (SEQ ID NO:1; lane 5) or control peptide (SEQ ID NO:9; lane 6). In contrast, peptide rVI in the absence of PKC activators induced PKC autophosphorylation to over 80% of the levels obtained for PKC alone in the presence of optimal concentration of PS, DG, and calcium (compare Fig. 8 lane 1 (control) with lane 4 (peptide rVI)).

H. Effects of peptides homologous to WD-40 regions of RACK1 on histone phosphorylation by β PKC.

Another measure of PKC activity is the ability of activated PKC enzyme to phosphorylate histones. PKC phosphorylation of histone was carried out using a modification of the protocol described by Mochly-Rosen, et al., (1987). Phosphorylation was carried out in the presence or absence of PKC activators (PS, DG and calcium) and RACK1-derived peptides. Phosphorylated histone was detected by autoradiography, following SDS-PAGE on a 10% gel.

Since peptide rVI (SEQ ID NO:7) was effective to induce the autophosphorylation of PKC in the absence of PKC activators, and both peptides rIII (SEQ ID NO:4) and rVI rendered PKC susceptible to proteolysis by Arg-C, experiments were performed to characterize the effect of the peptides on histone type III phosphorylation by PKC. The experiments are detailed in Example 11 and the results are shown in Figures 9 and 10.

The results are similar to those obtained for the effects of peptide rVI on autophosphorylation of PKC, that is, peptide rVI was effective to induce PKC-mediated histone phosphorylation in the absence of the PKC activators PS, DG, and calcium, once again supporting that peptide rVI is an agonist of PKC activation. Peptide rIII similarly induced histone phosphorylation (Fig. 10).

VIII. Utility.A. Peptides as probes for the identification of target proteins.

WD-40 derived peptides may be used, for example, to
5 isolate clones encoding target proteins from an expression
library. Variations on the cloning methods described herein can
be used to identify clones expressing sequences capable of
binding the peptides. For example, WD-40 derived peptides may
be used to detect a target protein on a membrane using a
10 standard binding assay. Positive clones may be detected, for
example, by radiolabeling the peptides and exposing the membrane
to film.

Target proteins isolated in this manner may be
completely novel, or they may be partially characterized (in
15 terms of a biological activity in a homogenate, or a band on a
protein gel, for example).

Upon isolation of a cDNA encoding a binding protein,
the cDNA may be expressed, for example, as detailed herein, and
the protein may be characterized. Purified protein thus
20 isolated may be used for a number of applications, including the
production of antibodies.

Peptides designed according a method of the present
invention may also be used, for example, as probes in a Western
blot of a tissue homogenate to identify and determine the
25 molecular weight of known or putative target proteins.

Screens such as those described above may be
facilitated by the modification of peptides used for screening
to incorporate any of a variety of reporter moieties. For
example, the peptides can be radiolabeled with ^{125}I .
30 Alternatively, the peptides can be modified with a sequence-tag
or a ligand for an affinity column by methods known to those
skilled in the art.

The peptides may also be modified to covalently cross-
link to their targets after binding, for example with any of
35 various affinity reagent for cross linking known to those
skilled in the art. This enables the isolation of target
proteins that bind the peptides relatively weakly.

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B. Peptides as substitutes for defective WD-40 containing proteins.

In cases where a WD-40 containing protein is implicated in a disease (see, for example Reiner, et al.), peptides derived from WD-40 regions of the defective protein may be used as substitutes, for example, to activate a target enzyme. Such an approach may be more feasible than attempting therapy with intact proteins. The approach has an additional advantage in that it does not require knowledge of the chromosomal location of the affected gene.

The peptides can be introduced into affected cells by any of several methods known to those skilled in the art, including through the use of an appropriate expression vector or through in vitro synthesis and administration by an effective, expedient route. In vitro studies can be carried out using skinning or microinjection techniques.

C. Peptides as pharmaceutical agents.

WD-40 derived peptides of the present invention may be used therapeutically, as described above. Such peptides may be designed so as to interact with endogenous target molecules to augment or correct their function. Alternatively, peptides may be designed to specifically interact with target molecules unique to a pathogenic organism.

D. Peptides as modulators of enzyme activity of proteins involved in protein-protein interactions.

Peptides synthesized according to a method of the invention may be effective to modulate the function of a target molecule (e.g. serve as agonists or antagonists). As shown herein, for example, peptides rVIII and rVI can serve to activate or enhance the activation of PKC, whereas peptide I can inhibit PKC.

These activities may be used in screens to identify other compounds which may affect the function of target molecules such as PKC. In particular, because WD-40 derived peptides may interact with PKC in a manner that is more similar to in vivo interactions (i.e. protein binding), they may be

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useful for identifying molecules or compounds that may interfere with PKC function *in vivo*, but might not necessarily interfere with PKC *in vitro*.

For example, peptide rVI can be used to stimulate PKC in the absence of traditional PKC activators, and the rVI-stimulated enzyme may be used in a screen to identify, for example, novel PKC-inhibiting or PKC-potentiating compounds.

If constitutive activation or inactivation of a target enzyme is desired, peptides may be designed with integrated or derivatized cross-linking moieties. The peptides can be cross-linked to their targets upon binding such that the target molecule assumes the desired state of activity for the lifetime of the target molecule.

Conversely, as described herein for PKC, peptides may also be designed so as to accelerate the degradation of the target molecule. For example, peptide rIII accelerated the degradation of PKC in cardiac myocytes.

E. WD-40 derived peptides as specific modulators of isozymes.

Peptides designed according to a method of the present invention can also be used to provide target isozyme-specific modulator molecules. For example, most cells have several PKC isozymes, all of which are activated by the same cellular stimuli. Determining the function of the individual isozymes is therefore difficult.

WD-40 derived peptides that selectively stimulate or inhibit specific target isozymes or groups of isozymes may be useful, both in terms of therapeutic value, and in terms of determining the roles of different isozymes in cellular function and disease. Such information can be useful for the identification of new molecular targets for drug development, as is described in part F, below.

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F. Compounds designed based on the predicted structure of binding peptides as pharmaceutical agents.

Peptides derived from WD-40 repeats may be useful for identifying lead compounds for drug development. Peptides as small as 7 residues have been shown herein to possess specific bioactivities upon interaction with their targets *in vivo*. The structure of such small peptides can be readily determined by a number of methods, such as NMR and X-ray crystallography. A comparison of the structures of peptides similar in sequence, but differing in the biological activities they elicit in the target molecules, can provide information about the structure-activity relationship (SAR) of the target enzyme.

For example, peptide I and RACK1-derived peptides rIII (SEQ ID NO:4) and rVI (SEQ ID NO:7) had opposite effect *in vivo*, although they are homologous in sequence.

Information gleaned from the examination of structure-activity relationships can be used to design either modified peptides, or other small molecules or lead compounds which can be tested for predicted properties (e.g. agonist or antagonist), as related to the target enzyme. The activity of the lead compounds can be evaluated using assays similar to those used in the evaluation of peptide-binding effects.

Information relating to a SAR of a target enzyme may also be obtained from co-crystallization studies. In such studies, a peptide with a desired activity is crystallized in association with a target protein, and the X-ray structure of the complex is determined. The structure can then be compared, for example, to the structure of the target protein in its native state, and information from such a comparison may be used to design compounds expected to possess specific activities. The compounds can be evaluated using assays similar to those used in the evaluation of peptide-binding effects.

G. PCR of cDNA corresponding to WD-40 repeats to identify mutations in WD-40 containing proteins.

Results presented herein suggest that the middle regions of WD-40 motifs are involved in the association of a WD-40 protein with its target protein. Because this association

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is likely to play a central role in the activity of a polypeptide complex comprised of interacting proteins, some genetic diseases may include mutations at these regions of WD-40 containing proteins. Therefore, if a WD-40 containing

5 protein is implicated in a genetic disorder, it may be possible to use PCR to amplify DNA from the WD-40 regions to quickly check if a mutation is contained within one of the WD-40 motifs. Primers can be made corresponding to either (i) the flanking regions of each repeat or (ii) the flanking regions of a series
10 of tandem repeats from the affected gene. Standard sequencing techniques can be used to determine whether a mutation is present. This method does not require prior chromosome mapping of the affected gene and can save time by obviating the need to sequence the entire gene encoding a defective WD-40 protein.

15 H. WD-40 based polypeptides as affinity ligands

Since the polypeptide compositions of the invention are able to bind proteins of interest, generically called a "first protein", the polypeptide compositions can also be used to retrieve the proteins of interest from samples and the
20 peptides can be used as affinity ligands for chromatographic procedures to purify and analyze said proteins. Standard chromatographic techniques are employed. Typically, the polypeptide is coupled to a solid support and the sample putatively containing the first protein is contacted with the
25 polypeptide composition of the invention; any unbound components of the sample are removed and, if desired, the first protein, bound to support, is eluted and recovered.

I. Use of peptides in screening tests for candidates

Various candidate compounds, not necessarily
30 polypeptides, may be shown to bind to a first protein using the polypeptides of the invention as competitors. In these screening assays, the ability of a candidate compound to bind a first protein can be assessed by contacting the first protein with the polypeptide composition of the invention in the
35 presence and absence of the candidate compound and evaluating the level of binding of the polypeptide in the presence as opposed to the absence of the candidate. Decreased binding of

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the polypeptide in the presence of the candidate indicates that the candidate binds to the first protein.

More broadly, the interaction of a protein with a polypeptide subsequence contained in the second protein can be assessed by contacting the first protein with a polypeptide representing the subsequence and observing any interaction with the polypeptide composition.

IX. Production of the Peptides of the Invention

The polypeptides of the invention can be prepared using standard techniques for the synthesis of peptides from amino acids. Such techniques, when conducted in solid phase chemistry are available commercially.

The polypeptides of the invention may also be produced using recombinant methods. These methods are by now well known in the art; DNA molecules containing nucleotide sequences encoding the desired polypeptides can readily be synthesized and ligated into expression systems for production of the peptides as is understood in the art. A wide variety of hosts is available, including procaryotic and eucaryotic hosts. The construction of expression vectors, means to modify these hosts, and culturing the modified hosts for recombinant production of polypeptides are conducted using standard techniques.

The following examples illustrate, but do not limit the present invention.

25 Materials and Methods

Nitrocellulose filters were obtained from Schleicher and Schuell (Keene, NH).

Synthetic peptides were prepared using commercially available automated peptide synthesizers. Alternatively, custom designed peptides may be purchased, for example, from Bachem Bioscience (King of Prussia, PA). Peptides may also be prepared recombinantly by expressing oligonucleotide sequences encoding the peptides. The oligonucleotide sequences may be either synthesized directly by standard methods of oligonucleotide synthesis, or, in the case of large coding sequences, synthesized by a series of cloning steps involving a tandem array of multiple oligonucleotide

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fragments corresponding to the coding sequence (Crea; Yoshio, et al.; Eaton, et al.). Oligonucleotide coding sequences can be expressed by standard recombinant procedures (Maniatis, et al.; Ausubel, et al.).

5 "Triton" refers to a nonionic detergent comprising a polyoxyethylene ether and other surface-active compounds. An exemplary Triton detergent is "TRITON X-100", available from Sigma Chemical Company, St. Louis, MO.

10 "Tween" refers to a nonionic detergent comprising polyoxyethylenesorbitan monolaurate with a fatty acid composition of approximately 55% lauric acid, with a balance composed primarily of myristic, palmitic and stearic acids. An exemplary Tween detergent is "TWEEN 20", available from Sigma Chemical Company, St. Louis, MO.

15 "SDS" refers to sodium dodecyl sulfate.

"PAGE" refers to polyacrylamide gel electrophoresis.

"IPTG" refers to isopropyl β -D-thiogalactopyranoside.

Example 1

Expression Cloning of a PKC-binding Protein

20 A. Buffers.

Overlay block buffer: 50 mM Tris-HCl (pH 7.5), 0.2 M NaCl, 3% bovine serum albumin (BSA) and 0.1% polyethylene glycol.

Overlay buffer: 50 mM Tris-HCl (pH 7.5), 0.2 M NaCl, 12 mM 2-mercaptoethanol, 0.1 % BSA, 1% polyethylene glycol, 10 μ g per
25 ml soybean trypsin inhibitor and 10 μ g per ml leupeptin.

B. Isolation of a PKC-binding cDNA clone by an overlay assay.

A rat brain (Sprague Dawley) cDNA expression library, constructed in the lambda phage cloning vector "UNI-ZAP XR"
30 (Stratagene, La Jolla, CA), was screened by an overlay assay as follows.

Lifts of nitrocellulose filters from IPTG-induced cDNA library plates were incubated for 2 hours in overlay block buffer. The filters were then transferred to overlay buffer with or without
35 1 unit of a mixture of rat brain PKC isozymes (α , β , γ , δ , ϵ and ζ , ~10 nM final concentration each) and incubated for 20 minutes

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at room temperature with PKC activators (60 μ g/ml phosphatidylserine (PS), 2 μ g/ml diacylglycerol (DG), 1 mM CaCl_2).

Following three 15 minute washes in the overlay buffer, the filters were incubated in the overlay block buffer in the presence of a mixture of monoclonal anti- α , β and γ PKC antibodies (1:1000 dilution; Seikagaku Kogyo, Tokyo, Japan) and polyclonal anti- δ , ϵ and ζ PKC antibodies (1:500 dilution; Life Technologies, Gaithersburg, MD). After a 16 hr incubation at room temperature, the filters were washed three times, 15 minutes per wash, in overlay buffer.

Binding of PKC was determined using alkaline phosphatase-conjugated goat anti-rabbit or goat anti-mouse antibodies (1:2000 dilution, Boehringer Mannheim Biochemicals, Indianapolis, IN). The alkaline phosphatase reaction used 5-bromo-4-chloro-3-indoyl phosphate p-toluidine salt as a substrate, and was performed following the manufacturer's protocol.

Library screening of 2.4×10^6 recombinant "UNI-ZAP" lambda phage plaques yielded one clone, pRACK1, that reacted with anti-PKC antibodies in the PKC overlay membrane, but not in the control overlay membrane. These results suggest that pRACK1 encodes a PKC binding protein.

C. Cloning and sequencing cDNA from positive plaques.

The clone pRACK1, identified as detailed in part B above, was plaque purified and cDNA inserts were isolated as phagemids by *in vivo* excision of the cloning vector, according to the manufacture's protocol (Stratagene, La Jolla, CA). DNA sequencing of pRACK1 was carried out using standard di-deoxy sequencing techniques (Maniatis, et al.) The DNA sequence of RACK1 is shown in Figure 1A. The sequence is also contained in the Sequence Listing as SEQ ID NO:19.

Example 2

Expression and Purification of Recombinant RACK1 Protein in *E. coli*

A PstI/XhoI DNA fragment containing an open reading frame of 317 amino acids from the putative translation start site of pRACK1 (see underlined ATG in Fig. 1A) and 8 additional nucleotides

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upstream of the initiating methionine was subcloned into *E. coli* expression vector pMAL-c2 (New England BioLabs, Beverly, MA). This vector contains the *malE* gene, which encodes maltose-binding protein (MBP). Induction of *E. coli* containing the vector results in the production of an MBP-fusion protein (Ausubel, et al.). The vector also includes a recognition site for the protease factor Xa, which allows the protein of interest to be cleaved from MBP after purification without adding any vector-derived residues to the protein.

A culture of TB1 *E. coli* transformed with RACK1-containing pMAL-c2 was induced by a 3 hr incubation with 1.8 mM IPTG. A protein fraction containing a 78 kDa fusion protein, comprised of RACK1 fused to MBP was isolated from the cultured *E. coli* by standard methods (Ausubel). The fusion protein was purified on an amylose affinity column according to the manufacture's protocol (New England BioLabs, Beverly, MA) and incubated with protease Xa (New England BioLabs) to yield a 36 kDa protein (RACK1) and a 34 kDa protein (possibly a RACK1 degradation product).

Example 3

Binding of PKC to Recombinant RACK1

A. Buffers.

PBS/Tween buffer: 140 mM NaCl, 8 mM Na₂PO₄, 1.5 mM KH₂PO₄, 3 mM KCl and 0.05% Tween at pH 7.0.

Overlay wash buffer: 50 mM Tris-HCl (pH 7.5), 0.2 M NaCl, 12 mM 2-mercaptoethanol, 0.1% polyethylene glycol and 0.1 mM CaCl₂.

B. Overlay assay.

Purified recombinant RACK1 protein (100-250 µg per lane, produced as detailed in Example 2) was subjected to SDS/PAGE and blotted onto nitrocellulose membranes (Ausubel). The nitrocellulose membranes were cut into strips, which were incubated for 0.5 hr in overlay buffer (Example 1) in the presence or absence of a mixture of PKC isozymes (α , β , γ , δ , ϵ and ζ , ~10 nM each final concentration) and PKC activators (60 µg/ml phosphatidylserine (PS), 2 µg/ml diacylglycerol (DG), and 1 mM CaCl₂). Unbound material was removed by five washes, 5-min each,

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in overlay wash buffer. Where indicated, PKC activators were present during the incubation of PKC with the nitrocellulose strips. The conditions for each sample and corresponding results are presented in part D below.

5 C. Detection of bound PKC.

PKC bound to RACK1 immobilized on nitrocellulose strips was detected as follows. The strips were incubated for 16 hours at room temperature with a mixture of anti-PKC antibodies as detailed in part B of Example 1, and then washed three times, 15 minutes per wash, with PBS/Tween buffer. The strips were incubated with anti-mouse and anti-rabbit horseradish peroxidase-linked secondary antibodies (Amersham Life Science, Arlington Heights, IL) diluted 1:1000 in PBS/Tween buffer supplements with 2% BSA, for 1 hour at room temperature. After washing three times, 15 minutes per wash with PBS/Tween buffer, the strips were subjected to a chemiluminescent reaction with luminol (diacylhydrazide) as detailed in the manufacturer's protocol (Amersham Life Science, Arlington Heights, IL), followed by an immediate exposure to autoradiography film (Eastman Kodak, Rochester, NY) for 30 seconds to 5 minutes.

D. Effects of PKC activation on PKC binding to RACK1.

The results presented in Figure 2 show the influence of PKC activators on the binding of PKC to RACK1 immobilized on nitrocellulose membranes. The overlay assay was carried out as described in part B above. The test reagents contained in each sample and the corresponding lanes on the blot presented in Fig. 2 are as follows. Lane 1: PKC, 60 μ g/ml PS, 2 μ g/ml DG and 1 mM CaCl_2 ; lane 2: PKC and 1 mM EGTA; lane 3: PKC, 60 μ g/ml PS and 2 μ g/ml DG; lane 4: PKC and 1 mM CaCl_2 ; lane 5: No PKC added; lanes 6 and 7: PKC, 60 μ g/ml PS 2 μ g/ml DG, 1 mM CaCl_2 , and 10 μ M substrate peptide (SEQ ID NO:11; lane 6) or 10 μ M pseudosubstrate peptide (SEQ ID NO:12; lane 7). The results are representative of three independent experiments.

It can be appreciated that the binding of PKC as detected by anti-PKC antibodies is minimal in the presence of EGTA or calcium alone (Fig. 2, lanes 2, 4, respectively), is greater in the

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presence of phosphatidylserine (PS) and diacylglycerol (DG; lane 3), and is maximal in the presence PS, DG and calcium (lane 1). Antibody binding was not observed in the absence of added PKC (lane 5). Furthermore, maltose binding protein alone, or an extract from 5 non-transformed *E. coli* did not bind PKC.

The concentration dependence of PKC binding to RACK1 was characterized with β PKC, since this isozyme is a major component of the PKC mixture used for the overlay assay. The mean half maximal binding was ~ 0.375 nM, and maximal binding was ~ 4 nM (n=3; 10 values reflect binding of β PKC isozyme in the presence of other PKC isozymes and was determined by scanning autoradiograms in the linear range of detection, as described in Mochly-Rosen, et al., (1991).

The results presented above indicate that in order for 15 PKC to bind to RACK1 it must be activated. In vitro, activation may be accomplished, for example, by phosphatidylserine and diacylglycerol, or, more preferably, by phosphatidylserine, diacylglycerol and calcium.

Example 4

20 Inhibition of PKC Binding to RACK1 by RACK1-specific WD-40-homologous Peptides

Assays for the inhibition of PKC binding to RACK1 by putative binding peptides were carried out by combining a variation of the overlay protocol described in Example 3 part B above, with 25 an overlay extraction assay described in part B below. The variation in the overlay protocol consisted of incubating the putative binding peptides with a mixture of PKC isozymes for 15 minutes at room temperature before the mixture was used to contact the nitrocellulose strips containing immobilized RACK1.

30 A. Buffers.

Sample buffer: 0.3 M Tris HCl, 5% SDS, 50% glycerol, 0.01% bromophenol blue and 5% β -mercaptoethanol.

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B. Overlay extraction protocol.

Nitrocellulose strips containing immobilized RACK1, that had been contacted with a solution containing a mixture of PKC isozymes, were washed and the area corresponding to the 36 kDa (RACK1-containing) band was cut out. The pieces (containing PKC/RACK1 complexes) were incubated with sample buffer for 10 minutes at 80°C. The sample buffer and the nitrocellulose pieces were then placed in wells in the PAGE gel and subjected to SDS-PAGE to elute the bound proteins. The gel was blotted onto nitrocellulose and a Western blot analysis was carried out using the mixture of antibodies (specific for PKC α , β , γ , δ , ϵ and ζ isozymes) described in Example 1 part B. Bound antibodies were detected by ^{125}I -protein A.

C. PKC overlay in the presence of binding peptides.

Peptides derived from or homologous to WD-40 repeats of RACK1 were tested for their ability to inhibit PKC binding to recombinant RACK1. Binding of PKC to RACK1 was carried out using a variation of the overlay procedure described in Example 3 part B. In the experimental samples, peptides were incubated with a solution containing a mixture of rat brain PKC isozymes (~10 nM each) for 15 minutes at room temperature.

Following completion of the modified overlay protocol, the samples were subjected to the overlay-extraction protocol detailed in part B, above.

The results in Figure 3 show the binding of PKC to RACK1, carried out without (lane 1) or with (lanes 2-4) a preincubation of peptides with PKC. Lane 2 shows PKC binding following a preincubation with 10 μM peptide I (SEQ ID NO:1). Peptide I caused an 81 \pm 6% inhibition of PKC binding to recombinant RACK1 as compared with binding in the absence of added peptide (n=3). Lanes 3 and 4 show PKC binding following a preincubation with 10 μM peptide rIII (SEQ ID NO:4) and 10 μM peptide rVI (SEQ ID NO:7), respectively. Both peptides inhibit the binding of PKC to RACK1. It can be seen that peptide rIII is somewhat more effective than peptide rVI. The results shown are representative of three independent experiments.

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The overlay-extraction method (part B above) was used in experiments relating to the peptide inhibition of PKC binding in order to decrease the possibility that some part of the inhibition of PKC binding to RACK1 reflects an interference in the binding of anti-PKC antibodies to the PKC/RACK1 complexes. Free peptides are effectively removed from the PKC/RACK1 complexes during the second round of SDS/PAGE, prior to blotting and detection of immobilized PKC/RACK1 complexes by anti-PKC antibodies.

Example 5

10 Identification of Sequenced Proteins Containing WD-40 Repeats

A search for WD-40 motif-containing proteins was done using the ENTREZ program, release 6.0 (National Center for Biotechnology Information, National Library of Medicine, National Institutes of Health, Bethesda, MD). The ENTREZ database was searched for protein sequences related to the β subunit of transducin.

Protein sequences homologous to β -transducin were examined for the existence of WD-40 repeats, following the guidance for identification of WD-40 repeats presented in section V of the specification, above.

The proteins were also used to carry out additional searches of the database, in order to identify other proteins which may contain WD-40 repeats, but which might not be homologous to the β subunit of transducin. Sequences identified during the second round of searches were again examined for WD-40 repeats.

This search strategy identified 30 proteins containing WD-40 sequences. The amino acid sequences of these proteins, with the WD-40 regions aligned and delineated, are shown in Figs. 12-18, 20-27, 29-30, 34-35, 37-38, 40 and 42-50. The sequences are represented in the Sequence Listing as SEQ ID NO:29-35, 37-44, 46-47, 51-52, 54-55, 57 and 59-67. An examination of the sequences in the figures reveals that although there can be divergence between the WD-40 motifs of different proteins, a consistent pattern can be inferred based on the teachings presented in part V of the specification above.

An additional search, using a consensus WD-40 sequence (SEQ ID NO:262), was conducted with the "MACVECTOR" program

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(Eastman Kodak Co., New Haven, CT) to search GenBank (December 1993 release). Default settings (matrix=250) were used for the search. The search identified the 250 proteins with the highest homology to the consensus sequence. These proteins were examined, as detailed in part V above, for WD-40 repeats. Ten additional proteins containing WD-40 repeats were identified with this strategy. The amino acid sequences of those proteins, with the WD-40 repeats aligned and delineated, are shown in Figs. 11, 19, 28, 31-33, 36, 39, 41 and 51. The sequences are represented in the Sequence Listing as SEQ ID NO:28, 36, 45, 48-50, 53, 56, 58 and 68.

Example 6

Binding of β PKC to RACK1 WD-40-derived Peptides

A. Buffers.

Peptide overlay block buffer: 20 mM Tris-HCl (pH 7.5), 0.2 M NaCl, 3% bovine serum albumin (BSA) and 0.1% polyethylene glycol.

Overlay wash buffer: 50 mM Tris-HCl (pH 7.5), 0.2 M NaCl, 12 mM 2-mercaptoethanol, 0.1% polyethylene glycol and 0.1 mM CaCl_2 .

B. PKC overlay of immobilized peptides.

The binding of β PKC to peptide I (SEQ ID NO:1), peptide rVI (SEQ ID NO:7) and control peptide (SEQ ID NO:9) was assessed using a PKC overlay assay similar to that described in Example 3. Increasing amounts of peptides (0.5 μ mole, 1.0 μ mole, 5.0 μ mole and 10.0 μ mole) suspended in 20 mM NaCl were applied individually onto nitrocellulose using a slot-blot apparatus (Schleicher and Schuell, Keene, NH). The nitrocellulose membrane was washed three times, 15 minutes per wash, in peptide overlay buffer and incubated for two hours in peptide overlay block buffer. The membrane was cut into sections and the sections were transferred to different PKC-containing solutions and incubated for 30 minutes at room temperature. All the solutions contained 5 nM rat brain PKC in peptide overlay buffer. Some solutions additionally contained PS, DG, and calcium. The membranes were then washed three times, 15 minutes per wash, in peptide overlay buffer and incubated in peptide overlay block buffer containing anti- β PKC monoclonal antibodies (1:1000 dilution; Seikagaku Kogyo, Tokyo, Japan). After

- 52 -

a 16 hr incubation at room temperature, the filters were washed three times, 15 minutes per wash, in peptide overlay buffer.

Binding of PKC was determined using chemiluminescence as described in Example 3, part C. Quantitation of PKC binding was carried out using a "MICRO SCAN" 1000 gel analyzer (Galai Inc., Yokneam, Israel).

The data show that activated PKC bound to both peptides I and rVI, but not to the control peptide, at peptide amounts as low as 5 μ moles. Unactivated PKC did not bind to peptide I, but did bind to peptide rVI at similar concentrations.

The results indicate that peptide rVI is capable of binding both activated as well as unactivated forms of PKC, whereas peptide I binds only to activated PKC.

Example 7

Effects of RACK1 WD-40-derived Peptides on PKC-mediated Oocyte Maturation

Exposure to insulin induces maturation in *Xenopus* oocytes via a PKC-dependent pathway (Smith, et al., 1992). The maturation response may be quantified by monitoring the appearance of a white spot in the animal hemisphere of the oocyte, indicating germinal vesicle breakdown (GVBD) and maturation. To assess the effects of RACK1 WD-40-derived peptides on insulin-induced PKC-mediated maturation, 50 nl of a 20 mM NaCl solution containing the indicated peptides [peptide I (SEQ ID NO:1; ●), peptide rVI (SEQ ID NO:7; ■), or injection solution (□)] (peptides at 50 μ M) were microinjected into *Xenopus* oocytes. The symbols refer to symbols used in Figure 5, which shows the data from this example. One hour following the peptide injections, the oocytes were exposed to a solution containing insulin (8.25 μ g/ml) for 2 minutes (t=0). 10-15 oocytes were used for each sample.

The data, representative of three independent experiments, are expressed as the percent of oocytes with GVBD following insulin exposure and are plotted as a function of time in Figure 5.

In oocytes injected with buffer or control peptide, onset of maturation was typically 4-5 hours after exposure to insulin. Following this delay, %GVBD followed an approximately exponential

- 53 -

time-course, reaching a plateau of about 85-90% GVBD at about 10-12 hours. These data indicate that approximately 80-85% of sham-injected oocytes exposed to insulin at $t=0$ reach maturation, and that maturation is reached relatively quickly (within about 10 hours) relative to the time-course of the experiment (20 hours).

Oocytes injected with peptide I (SEQ ID NO:1) responded in a manner similar to control oocytes, except the plateau was at about 45-50% GVBD. These data suggest that injection of peptide I blocked maturation in approximately 40-45% of oocytes that would normally proceed to maturation, but had little effect on the kinetics or extent of maturation of the remaining (50-55%) oocytes.

Oocytes injected with peptide rVI (SEQ ID NO:7) responded with a slightly shorter delay (about 3-4 hours), but reached a higher plateau (about 95-100% GVBD) more quickly (within about 5 hours) than control oocytes. These data suggest that peptide rVI potentiates the effects of insulin on oocyte maturation, both in terms of the rate of maturation, and in the total fraction of oocytes that mature during the experiment. Injection of peptide rVI increases the maturing fraction to essentially 100%.

The effects of both peptides I and rVI on GVBD were dose-dependent between 5 μM -500 μM .

Since peptide rVI enhanced insulin-induced GVBD, experiments were performed to determine whether peptide rVI can induce GVBD in the absence of insulin. The data from these experiments are shown in Fig. 5B. Microinjection of peptide rVI (50 μM) alone, but not peptide I, control peptide or buffer, induced GVBD. Maturation initiated with a longer delay (about 6-7 hours) than in the control insulin-induced oocytes in Fig. 5A (about 4-5 hours), and reached a plateau of about 50% GVBD.

Together, the data above indicate that peptides homologous to the WD-40 region of RACK1 modulate the function of PKC. Peptide I inhibited PKC-mediated oocyte maturation by about 40%, whereas peptide rVI potentiated insulin-induced maturation, and resulted in a limited maturation response even in the absence of insulin. The latter result suggests that peptide rVI, under appropriate circumstances, may act to activate PKC in the absence of other activating substances.

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Example 8Effects of RACK1 WD-40-derived Peptides on PKC Translocation in
Xenopus OocytesA. Buffers.

5 Homogenization buffer: 20 mM Tris HCl, pH 7.5, 10 mM EGTA, 2 mM EDTA, 0.25M sucrose, 10 μ M phenylmethylsulfonyl fluoride, 20 μ g/ml of each leupeptin and soybean trypsin inhibitor.

B. PKC translocation in oocytes.

10 Insulin causes the translocation of β PKC, but not other PKC isozymes, from a cytosolic form to a membrane-associated form, as evidenced by the relative levels of PKC in the soluble vs. the particulate fraction of oocyte homogenate. To assess the effects of RACK1 WD-40-derived peptides on insulin-induced PKC translocation, 50 nl of a 20 mM NaCl solution containing the
15 indicated peptides were microinjected into *Xenopus* oocytes. The oocytes were then homogenized, and the relative amount of PKC in the soluble and particulate fractions was assayed. The protocol followed was a modification of a method described by Smith, et al. (1992). The results are shown in Figure 6.

20 Batches of 50 oocytes were microinjected with either peptide rVI (SEQ ID NO:7; 50 μ M; lanes 3, 4), peptide I (SEQ ID NO:1; 50 μ M, lanes 7, 8) or injection solution (NaCl 20 mM, lanes 1,2 and 5,6). Homogenates from each batch were prepared 60 minutes after microinjection (lanes 1-4) or 60 minutes after
25 addition of insulin (lanes 5-8). The homogenates were centrifuged at 10,000 g for 3 minutes, the upper layer (containing fat and yolk) was removed, and the remainder was frozen at -70 °C. Prior to use, the samples were thawed, 200 μ l homogenization buffer was added and the samples were centrifuged at 100,000 g for 30 minutes
30 at 4 °C. The supernatants (soluble fraction) were removed and concentrated to 20 μ l using "CENTRICON" concentrators (Amicon, Beverly, MA). The pellets (particulate fractions) were dissolved in 20 μ l of homogenization buffer. The samples were resolved on an 8% SDS/PAGE gel and blotted onto nitrocellulose.
35 The amount of PKC in each fraction was determined by Western blot using anti- β PKC antibodies (1:1000 dilution; Seikagaku Kogyo,

- 55 -

Tokyo, Japan). Bound primary antibodies were detected by chemiluminescence as described in Example 3, part C.

The antibodies showed immunoreactivity with an ~80 kDa protein that corresponds to β PKC. Data are representative of three experiments.

The data are shown in Figure 6. Lanes 1, 3, 5 and 7 contain particulate fractions (p), while lanes 2, 4, 6 and 8 contain soluble (cytosol) fractions (c). Peptide I (50 μ M) did not affect β PKC distribution in untreated oocytes, but inhibited insulin-induced β PKC translocation (Fig. 3, lanes 7,8). In contrast, peptide rVI (50 μ M) induced β PKC translocation in the absence of insulin treatment (Fig. 3, lanes 3,4).

The results above suggest that peptide I is an antagonist of insulin-induced PKC translocation, whereas peptide rVI is an agonist and an activator of PKC translocation. In light of the results presented in Example 7, the data also suggest that the inhibition of insulin-induced GVBD following microinjection of peptide I was due to an inhibition of β PKC translocation.

Example 9

20 Effects of RACK1 WD-40-derived Peptides on Sensitivity of PKC to Arg-C Endopeptidase

A. Buffers.

Sample buffer: 0.3 M Tris HCl, 5% SDS, 50% glycerol, 0.01% bromophenol blue and 5% β -mercaptoethanol.

25 B. Nicking of β PKC by Arg-C endopeptidase.

Upon activation of PKC, a pseudosubstrate autoinhibitory sequence at the N-terminus of the molecule dissociates from the catalytic site and becomes sensitive to endopeptidase Arg-C (Orr, et al.). In the absence of PKC activators, exposure of the 80 kDa β PKC to endopeptidase Arg-C has no effect on the enzyme (see Fig 7, lane 1). In the presence of the PKC activators PS, DG and calcium, however, exposure of β PKC to Arg-C results in a "nicking" of the PKC (i.e. limited proteolysis generating a 78 kDa fragment and several small fragments (see Fig. 7, lane 2)). Continued exposure to Arg-C results in the disappearance of β PKC (Orr, et al.). The present experiment tests whether peptides derived from

- 56 -

the WD-40 region of RACK1 alter the sensitivity of β PKC to endopeptidase Arg-C.

The methods used to assay Arg-C sensitivity are a modification of methods described by Orr, et al. Rat brain PKC (~ 5 nM) was incubated at room temperature in 500 μ l of 20 mM Tris-HCl buffer (pH 7.5) alone or with Arg-C (5 units/ml) in the presence or absence of the indicated peptides (final concentration 10 μ M or as indicated), PS, DG, and calcium (as indicated). 50 μ l aliquots were removed into 20 μ l of sample buffer during the reaction as indicated (samples in all the lanes were incubated for 30 minutes, except lanes 5, and 6, which were incubated for 5 and 15 minutes, respectively). The samples were boiled for 10 minutes at 80°C and loaded onto 8% SDS-PAGE. β PKC was detected by Western blot analysis using anti- β PKC antibodies as described in Examples 6 and 8.

The results are shown in Figure 7. PKC was incubated for the indicated time alone (lane 1) or in the presence of Arg-C (lanes 2-9), with DG (0.8 μ g/ml), PS (50 μ g/ml) and CaCl_2 (1 mM; lane 2), with PS (50 μ g/ml) and CaCl_2 (1 mM; lane 3), with PS (2.5 μ g/ml) and CaCl_2 (50 μ M; lane 4); with PS (2.5 μ g/ml), CaCl_2 (50 μ M) and with either peptide rVI (SEQ ID NO:7; 10 μ M; lanes 5-7), control peptide (SEQ ID NO:9; lane 8) or with peptide I (SEQ ID NO:1; lane 9).

Incubation of β PKC with Arg-C at low concentrations of activators (2.5 μ g/ml PS and 50 μ M CaCl_2) in the absence of added peptide did not result in appreciable nicking activity (Fig. 7, lane 4). Similarly, nicking of β PKC did not occur in the presence of this concentration of activators with peptide I (lane 9) or with control peptide (lane 8). However, incubation of β PKC with the same concentration of activators in the presence of peptide rVI resulted in a time-dependent appearance of the 78 kDa nicked PKC fragment (Fig. 4, lanes 5-7). Concentrations as low as 10 nM of peptide rVI were sufficient to result in nicking activity, indicative of β PKC activation. The results indicate that peptide rVI, but not peptide I, is effective to stabilize PKC in an activated conformation that renders it susceptible to Arg-C under conditions of low PKC activators that would otherwise not render the enzyme susceptible to Arg-C.

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Example 10Effects of RACK1 WD-40-derived Peptides on PKCAutophosphorylation

Activated PKC is capable of autophosphorylation. Since
5 peptide rVI (SEQ ID NO:7) was effective to induce PKC translocation
and GVBD in the absence of an activator such as insulin, the
ability of the peptide to induce PKC autophosphorylation in the
absence of PKC activators was assessed.

PKC autophosphorylation in the presence of β PKC
10 pseudosubstrate antibodies or the indicated peptides was carried
out using a modification of the method described by Makowske, et
al. Anti-pseudosubstrate antibodies, which were shown previously
to induce autophosphorylation in the absence of PKC activators
(Makowske, et al.) were used as a positive control. The results
15 are shown in Figure 8.

Rat brain PKC (~ 10 nM) was incubated with mild agitation
in a final volume of 250 μ l of overlay buffer, as in Example 1
either with anti- β PKC pseudosubstrate antibodies (1:10 dilution,
Life Technologies, Gaithersburg, MD) or with the indicated peptide
20 (10 μ M). Where indicated, PS (50 μ g/ml), DG (0.8 μ g/ml) and CaCl_2
(1 mM) were also added. The amount of autophosphorylation was
determined after 2 hours for the reaction with the anti-
pseudosubstrate antibodies, or after 15 minutes for the other
samples. 50 μ l of a buffer comprised of 20 mM Tris-HCl (pH 7.5),
25 20 mM MgCl_2 , 20 μ M ATP and 5 μ ci/ml [γ - 32 P]ATP. The mixture was
incubated for 15 minutes at room temperature and the reaction was
stopped by adding 60 μ l sample buffer (see Example 9). The samples
were then boiled for 10 minutes, loaded onto a 10% SDS-PAGE mini
gel and electrophoresed. The gel was fixed with 50% methanol and
30 10% acetic acid for 1 hour, and the autophosphorylation of PKC was
determined by autoradiography.

The results in Figure 8 show PKC autophosphorylation in
the presence of DG, PS, and calcium (lane 1), in the presence of
EGTA (lane 2), in the presence of anti- β PKC pseudosubstrate
35 antibodies (diluted 1:10 in 20 mM Tris-HCl; lane 3), in the
presence of peptide rVI (SEQ ID NO:7; 10 μ M; lane 4), in the
presence of peptide I (SEQ ID NO:1; 10 μ M; lane 5), or in the
presence of control peptide (SEQ ID NO:9; 10 μ M; lane 6).

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Peptide rVI in the absence of PKC activators induced PKC autophosphorylation to over 80% of the autophosphorylation obtained in the presence of optimal concentration of PS, DG, and calcium (compare Fig. 8 lane 1 (control) with lane 4 (peptide rVI)).

5 Neither peptide I nor control peptide induced PKC autophosphorylation in the absence of PKC activators (Fig. 8 lanes 5 and 6, respectively).

Example 11

Effects of RACK1 WD-40-derived Peptides on Histone

10

Phosphorylation by PKC

Incubation of PKC with peptide rVI (SEQ ID NO:7) induced histone phosphorylation by PKC. The method used was a modification of the protocol described by Mochly-Rosen, et al. (1987). The results are shown in Figure 9.

15

Histone type IIIs (Sigma Chemical Company, St. Louis, MO) was phosphorylated by PKC (~ 10 nM) in the absence (lane 1) and presence of peptide rVI (10 μ M) (lanes 2 and 3) and in the presence and absence of DG (0.8 μ g/ml), PS (50 μ g/ml) and CaCl_2 (1 mM) (lane 3). The results are expressed as percentage of control that

20 is the amount of Histone phosphorylation by PKC in the presence of DG (0.8 μ g/ml), PS (50 μ g/ml) and CaCl_2 (1 mM). The results are the average \pm SEM of two independent experiments. PKC was first incubated with the peptide rVI (10 μ M) for 15 minutes in overlay buffer as described above. Histone type IIIs (40 μ g/ml) was added

25 in Tris-HCl (20 mM), MgCl_2 (20 mM), ATP (20 μ M) and [γ - 32 P]ATP (5 μ ci/ml) with or without PS (50 μ g/ml), DG (0.8 μ g/ml) and CaCl_2 (1 mM). Histone phosphorylation was determined by autoradiography as above.

PKC activators PS, DG, and calcium were not required for

30 either peptide rVI-induced autophosphorylation or histone phosphorylation, suggesting that peptide rVI is an agonist of PKC activation.

In a related experiment, phosphorylation of histone type IIIs (25 μ M) by PKC (10 nM) was not inhibited by RACK1; rather, a

35 4.5 \pm 0.1 fold increase of histone phosphorylation occurred when co-incubated with ~100 nM RACK1 (n=2).

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SEQUENCE LISTING

(1) GENERAL INFORMATION:

5

(i) APPLICANT: Mochly-Rosen, Daria
Ron, Dorit

10

(ii) TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
Thereof

(iii) NUMBER OF SEQUENCES: 265

15

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20

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

25

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: 08/190,802
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30

(viii) ATTORNEY/AGENT INFORMATION:

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35

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40

(2) INFORMATION FOR SEQ ID NO:1:

45

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 amino acids

- 60 -

(B) TYPE: amino acid
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

5

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

10

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Peptide I

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

15

Lys Gly Asp Tyr Glu Lys Ile Leu Val Ala Leu Cys Gly Gly Asn
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:2:

20

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 7 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: unknown

25

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

30

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Peptide, rI, Fig. 1C

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Val Thr Gln Ile Ala Thr Thr
1 5

40

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 7 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: unknown

45

- 61 -

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

5 (iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Peptide rII, Fig. 1C

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Phe Val Ser Asp Val Val Ile

1

5

15

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 7 amino acids

20

(B) TYPE: amino acid

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

25

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

30

(C) INDIVIDUAL ISOLATE: Peptide rIII, Fig. 1C

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

35

Asp Val Leu Ser Val Ala Phe

1

5

(2) INFORMATION FOR SEQ ID NO:5:

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 7 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: unknown

45

(ii) MOLECULE TYPE: peptide

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(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

5 (vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: peptide rIV, Fig. 1C

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

10

Val Ser Cys Val Arg Phe Ser
1 5

(2) INFORMATION FOR SEQ ID NO:6:

15

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 7 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: unknown

20

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

25 (iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Peptide rV, Fig. 1C

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Gly Tyr Leu Asn Thr Val Thr
1 5

35

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 8 amino acids

40

(B) TYPE: amino acid

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

45

(iii) HYPOTHETICAL: NO

- 63 -

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Peptide rVI, Fig. 1C

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Asp Ile Ile Asn Ala Leu Cys Phe
10 1 5

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 7 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

20

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

25 (vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Peptide rVII, Fig. 1C

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

30

Pro Gln Cys Thr Ser Leu Ala
1 5

(2) INFORMATION FOR SEQ ID NO:9:

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 6 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: unknown

40

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

45 (iv) ANTI-SENSE: NO

- 64 -

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: control peptide 1, homol. to RACK1
261-266, LKGKIL

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Leu Lys Gly Lys Ile Leu
1 5

10

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 6 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: unknown

15

(ii) MOLECULE TYPE: peptide

20

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

25

(C) INDIVIDUAL ISOLATE: control peptide 2, iden. to RACK1,
265 to 270 IIVDEL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

30

Ile Ile Val Asp Glu Leu
1 5

(2) INFORMATION FOR SEQ ID NO:11:

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: unknown

40

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

45

(iv) ANTI-SENSE: NO

- 65 -

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: PKC substrate peptide, (Ser25)
PKC(19-36)

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Arg Phe Ala Arg Lys Gly Ser Leu Arg Gln Lys Asn Val His Glu Val
1 5 10 15

10

Lys Asn

(2) INFORMATION FOR SEQ ID NO:12:

15

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: unknown

20

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

25

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: PKC Pseudosubstrate Inhibitor
(PCK(19-36))

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Arg Phe Ala Arg Lys Gly Ala Leu Arg Gln Lys Asn Val His Glu Val
35 1 5 10 15

Lys Asn

40 (2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 amino acids

(B) TYPE: amino acid

45

(D) TOPOLOGY: unknown

- 66 -

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

5 (iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: GBH Peptide, rI, Fig. 24

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Trp Val Thr Gln Ile Ala Thr Thr Pro Gln Phe Pro Asp Met Ile
1 5 10 15

15 (2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 amino acids

(B) TYPE: amino acid

20 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

25

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: GBH Peptide rII, Fig. 24

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Phe Val Ser Asp Val Val Ile Ser Ser Asp Gly Gln Phe Ala Leu
35 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 15 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

45

(iii) HYPOTHETICAL: NO

- 67 -

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: GBH Peptide rIII, Fig. 24

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Asp Val Leu Ser Val Ala Phe Ser Ser Asp Asn Arg Gln Ile Val
1 5 10 15

10

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 amino acids

15

(B) TYPE: amino acid

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

20

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

25

(C) INDIVIDUAL ISOLATE: GBH Peptide rIV, Fig. 24

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

30

Trp Val Ser Cys Val Arg Phe Ser Pro Asn Ser Ser Asn Pro Ile
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:17:

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: unknown

40

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

45

(vi) ORIGINAL SOURCE:

- 68 -

(C) INDIVIDUAL ISOLATE: GBH Peptide rV, Fig. 24

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

5 Tyr Leu Asn Thr Val Thr Val Ser Pro Asp Gly Ser Leu Cys Ala
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:18:

10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 15 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: unknown

15 (ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

20

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: GBH Peptide rVI, Fig. 24

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

 Thr Leu Asp Gly Gly Asp Ile Ile Asn Ala Leu Cys Phe Ser Pro
 1 5 10 15

30 (2) INFORMATION FOR SEQ ID NO:19:

 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1115 base pairs
 (B) TYPE: nucleic acid
35 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

40 (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

45 (C) INDIVIDUAL ISOLATE: RACK1 DNA Sequence, Fig. 1A

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GGCACGAGGG GTCGCGGTGG CAGCCGTGCG GTGCTTGGCT CCCTAAGCTA TCCGGTGCCA
60
5 TCCTTGTGCG TCGGCGGACT CGCAACATCT GCAGCCATGA CCGAGCAAAT GACCCTTCGT 120
GGGACCCTCA AGGGCCATAA TGGATGGGTT ACACAGATCG CCACCACTCC GCAGTTCCCG 180
10 GACATGATCC TGTGGCGTC TCGAGACAAG ACCATCATCA TGTGGAAGCT GACCAGGGAT 240
GAGACCAACT ACGGCATACC ACAACGTGCT CTTGAGGTC ACTCCCACTT TGTAGCGAT 300
GTTGTCATCT CCTCTGATGG CCAGTTTGCC CTCTCAGGCT CCTGGGATGG AACCTACGC 360
15 CTCTGGGATC TCACAACGGG CACTACCACG AGACGATTG TCGGCCACAC CAAGGATGTG 420
CTGAGCGTGG CTTTCTCCTC TGACAACCGG CAGATTGTCT CTGGGTCCCG AGACAAGACC 480
20 ATTAAGTTAT GGAATACTCT GGGTGTCTGC AAGTAACTG TCCAGGATGA GAGTCATTCA 540
GAATGGGTGT CTTGTGTCCG CTTCTCCCCG AACAGCAGCA ACCCTATCAT CGTCTCCTGC 600
GGATGGGACA AGCTGGTCAA GGTGTGGAAT CTGGCTAACT GCAAGCTAAA GACCAACCAC 660
25 ATTGGCCACA CTGGCTATCT GAACACAGTG ACTGTCTCTC CAGATGGATC CCTCTGTGCT 720
TCTGGAGGCA AGGATGGCCA GGCTATGCTG TGGGATCTCA ATGAAGGCAA GCACCTTTAC 780
30 ACATTAGATG GTGGAGACAT CATCAATGCC TTGTGCTTCA GCCCCAACCG CTAAGGCTC 840
TGTGCTGCCA CTGGCCCCAG TATCAAGATC TGGGACTTGG AGGGCAAGAT CATGGTAGAT 900
GAACTGAAGC AAGAAGTTAT CAGCACCAGC AGCAAGGCAG AGCCACCCCA GTGTACCTCT 960
35 TTGGCTTGGT CTGCTGATGG CCAGACTCTG TTTGCTGGCT ATACCGACAA CTTGGTGCGT 1020
GTATGGCAGG TGACTATTGG TACCCGCTAA AAGTTTATGA CAGACTCTTA GAAATAAACT 1080
40 GGCTTCTGA AAAAAAAAAA AAAAAAAAAA AAAAA 1115

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 96 base pairs
(B) TYPE: nucleic acid

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(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

5

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

10

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: RACK1 rI DNA Sequence, Fig. 1A

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

15

GGCCATAATG GATGGGTAC ACAGATCGCC ACCACTCCGC AGTTCCCGGA CATGATCCTG
60

TCGGCGTCTC GAGACAAGAC CATCATCATG TGAAG

20 96

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

25

(A) LENGTH: 94 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

30

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

35

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: RACK1 rII DNA Sequence

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

GGTCACTCCC ACTTTGTTAG CGATGTTGTC ATCTCCTCTG ATGGCCAGTT TGCCCTCTCA
60

45 GGCTCCTGGG ATGGAACCCT ACGCCTCTGG GATC

94

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(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 93 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

10

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

15

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: RACK1 rIII DNA Sequence, Fig. 1A

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

20

GGCCACACCA AGGATGTGCT GAGCGTGGCT TTCTCCTCTG ACAACCGGCA GATTGTCTCT
60

GGGTCCCGAG ACAAGACCAT TAAGTTATGG AAT

25

93

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 99 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

40

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: RACK1 rIV DNA Sequence, Fig. 1A

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

- 72 -

AGTCATTGAG AATGGGTGTC TTGTGTCCGC TTCTCCCCGA ACAGCAGCAA CCCTATCATC
60

GTCTCCTGCG GATGGGACAA GCTGGTCAAG GTGTGGAAT
5 99

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
- 10 (A) LENGTH: 93 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear
- 15 (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- 20 (vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: RACK1 rV DNA Sequence, Fig. 1A
- 25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

GGCCACACTG GCTATCTGAA CACAGTGACT GTCTCTCCAG ATGGATCCCT CTGTGCTTCT
60

30 GGAGGCAAGG ATGGCCAGGC TATGCTGTGG GAT
93

(2) INFORMATION FOR SEQ ID NO:25:

- 35 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 93 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear
- 40 (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- 45 (iv) ANTI-SENSE: NO

- 73 -

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: RACK1 rVI DNA Sequence, Fig. 1A

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

TTAGATGGTG GAGACATCAT CAATGCCTTG TGCTTCAGCC CCAACCGCTA CTGGCTCTGT
60

10 GCTGCCACTG GCCCCAGTAT CAAGATCTGG GAC
93

(2) INFORMATION FOR SEQ ID NO:26:

15 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 99 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

20

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

25 (iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: RACK1 rVII DNA Sequence, Fig. 1A

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

AGCAAGGCAG AGCCACCCCA GTGTACCTCT TTGGCTTGGT CTGCTGATGG CCAGACTCTG
60

35

TTTGCTGGCT ATACCGACAA CTTGGTGCGT GTATGGCAG
99

(2) INFORMATION FOR SEQ ID NO:27:

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 317 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: unknown

45

(ii) MOLECULE TYPE: protein

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(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

5 (vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: RACK1 Amino Acid Sequence, Fig. 1C

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

10

Met Thr Glu Gln Met Thr Leu Arg Gly Thr Leu Lys Gly His Asn Gly
 1 5 10 15

15

Trp Val Thr Gln Ile Ala Thr Thr Pro Gln Phe Pro Asp Met Ile Leu
 20 25 30

Ser Ala Ser Arg Asp Lys Thr Ile Ile Met Trp Lys Leu Thr Arg Asp
 35 40 45

20

Glu Thr Asn Tyr Gly Ile Pro Gln Arg Ala Leu Arg Gly His Ser His
 50 55 60

Phe Val Ser Asp Val Val Ile Ser Ser Asp Gly Gln Phe Ala Leu Ser
 65 70 75 80

25

Gly Ser Trp Asp Gly Thr Leu Arg Leu Trp Asp Leu Thr Thr Gly Thr
 85 90 95

30

Thr Thr Arg Arg Phe Val Gly His Thr Lys Asp Val Leu Ser Val Ala
 100 105 110

Phe Ser Ser Asp Asn Arg Gln Ile Val Ser Gly Ser Arg Asp Lys Thr
 115 120 125

35

Ile Lys Leu Trp Asn Thr Leu Gly Val Cys Lys Tyr Thr Val Gln Asp
 130 135 140

40

Glu Ser His Ser Glu Trp Val Ser Cys Val Arg Phe Ser Pro Asn Ser
 145 150 155 160

Ser Asn Pro Ile Ile Val Ser Cys Gly Trp Asp Lys Leu Val Lys Val
 165 170 175

45

Trp Asn Leu Ala Asn Cys Lys Leu Lys Thr Asn His Ile Gly His Thr
 180 185 190

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Gly Tyr Leu Asn Thr Val Thr Val Ser Pro Asp Gly Ser Leu Cys Ala
 195 200 205

Ser Gly Gly Lys Asp Gly Gln Ala Met Leu Trp Asp Leu Asn Glu Gly
 5 210 215 220

Lys His Leu Tyr Thr Leu Asp Gly Gly Asp Ile Ile Asn Ala Leu Cys
 225 230 235 240

Phe Ser Pro Asn Arg Tyr Trp Leu Cys Ala Ala Thr Gly Pro Ser Ile
 10 245 250 255

Lys Ile Trp Asp Leu Glu Gly Lys Ile Ile Val Asp Glu Leu Lys Gln
 260 265 270

Glu Val Ile Ser Thr Ser Ser Lys Ala Glu Pro Pro Gln Cys Thr Ser
 15 275 280 285

Leu Ala Trp Ser Ala Asp Gly Gln Thr Leu Phe Ala Gly Tyr Thr Asp
 20 290 295 300

Asn Leu Val Arg Val Trp Gln Val Thr Ile Gly Thr Arg
 305 310 315

25

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 501 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

35 (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

40 (C) INDIVIDUAL ISOLATE: Human 55 kDa protein (PWP homolog),
 Fig. 11

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

45 Met Asn Arg Ser Arg Gln Val Thr Cys Val Ala Trp Val Arg Cys Gly

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1	5	10	15
Val Ala Lys Glu Thr Pro Asp Lys Val Glu Leu Ser Lys Glu Glu Val	20	25	30
5	Lys Arg Leu Ile Ala Glu Ala Lys Glu Lys Leu Gln Glu Glu Gly Gly	35	40 45
10	Gly Ser Asp Glu Glu Glu Thr Gly Ser Pro Ser Glu Asp Gly Met Gln	50	55 60
	Ser Ala Arg Thr Gln Ala Arg Pro Arg Glu Pro Leu Glu Asp Gly Asp	65	70 75 80
15	Pro Glu Asp Asp Arg Thr Leu Asp Asp Asp Glu Leu Ala Glu Tyr Asp	85	90 95
	Leu Asp Lys Tyr Asp Glu Glu Gly Asp Pro Asp Ala Glu Thr Leu Gly	100	105 110
20	Glu Ser Leu Leu Gly Leu Thr Val Tyr Gly Ser Asn Asp Gln Asp Pro	115	120 125
	Tyr Val Thr Leu Lys Asp Thr Glu Gln Tyr Glu Arg Glu Asp Phe Leu	130	135 140
25	Ile Lys Pro Ser Asp Asn Leu Ile Val Cys Gly Arg Ala Glu Gln Asp	145	150 155 160
30	Gln Cys Asn Leu Glu Val His Val Tyr Asn Gln Glu Glu Asp Ser Phe	165	170 175
	Tyr Val His His Asp Ile Leu Leu Ser Ala Tyr Pro Leu Ser Val Glu	180	185 190
35	Trp Leu Asn Phe Asp Pro Ser Pro Asp Asp Ser Thr Gly Asn Tyr Ile	195	200 205
	Ala Val Gly Asn Met Thr Pro Val Ile Glu Val Trp Asp Leu Asp Ile	210	215 220
40	Val Asp Ser Leu Glu Pro Val Phe Thr Leu Gly Ser Lys Leu Ser Lys	225	230 235 240
45	Lys Lys Lys Lys Lys Gly Lys Lys Ser Ser Ser Ala Glu Gly His Thr	245	250 255

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[illegible]

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500

(2) INFORMATION FOR SEQ ID NO:29:

5 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 428 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: unknown

10 (ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

15

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: AAC-RICH protein, Fig. 12

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

Pro Gly Gly Phe Gln His Leu Gln Gln Gln Gln Gln Gln Gln Gln
 1 5 10 15

25 Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Thr Gln Val Gln
 20 25 30

Gln Leu His Asn Gln Leu His Gln Gln His Asn Gln Gln Ile Gln Gln
 35 40 45

30

Gln Ala Gln Ala Thr Gln Gln His Leu Gln Thr Gln Gln Tyr Leu Gln
 50 55 60

35

Ser Gln Ile His Gln Gln Ser Gln Gln Ser Gln Leu Ser Asn Asn Leu
 65 70 75 80

Asn Ser Asn Ser Lys Glu Ser Thr Asn Ile Pro Lys Thr Asn Thr Gln
 85 90 95

40

Tyr Thr Asn Phe Asp Ser Lys Asn Leu Asp Leu Ala Ser Arg Tyr Phe
 100 105 110

Ser Glu Cys Ser Thr Lys Asp Phe Ile Gly Asn Lys Lys Lys Ser Thr
 115 120 125

45

Ser Val Ala Trp Asn Ala Asn Gly Thr Lys Ile Ala Ser Ser Gly Ser

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	130	135	140
	Asp Gly Ile Val Arg Val Trp Asn Phe Asp Pro Leu Gly Asn Ser Asn		
	145	150	155 160
5	Asn Asn Asn Asn Ser Asn Asn Thr Ser Ser Asn Ser Lys Asn Asn Asn		
	165	170	175
	Ile Lys Glu Thr Ile Glu Leu Lys Gly His Asp Gly Ser Ile Glu Lys		
10	180	185	190
	Ile Ser Trp Ser Pro Lys Asn Asn Asp Leu Leu Ala Ser Ala Gly Thr		
	195	200	205
15	Asp Lys Val Ile Lys Ile Trp Asp Val Lys Ile Gly Lys Cys Ile Gly		
	210	215	220
	Thr Val Ser Thr Asn Ser Glu Asn Ile Asp Val Arg Trp Ser Pro Asp		
	225	230	235 240
20	Gly Asp His Leu Ala Leu Ile Asp Leu Pro Thr Ile Lys Thr Leu Lys		
	245	250	255
	Ile Tyr Lys Phe Asn Gly Glu Glu Leu Asn Gln Val Gly Trp Asp Asn		
25	260	265	270
	Asn Gly Asp Leu Ile Leu Met Ala Asn Ser Met Gly Asn Ile Glu Ala		
	275	280	285
30	Tyr Lys Phe Leu Pro Lys Ser Thr Thr His Val Lys His Leu Lys Thr		
	290	295	300
	Leu Tyr Gly His Thr Ala Ser Ile Tyr Cys Met Glu Phe Asp Pro Thr		
	305	310	315 320
35	Gly Lys Tyr Leu Ala Ala Gly Ser Ala Asp Ser Ile Val Ser Leu Trp		
	325	330	335
	Asp Ile Glu Asp Met Met Cys Val Lys Thr Phe Ile Lys Ser Thr Phe		
40	340	345	350
	Pro Cys Arg Ser Val Ser Phe Ser Phe Asp Gly Gln Phe Ile Ala Ala		
	355	360	365
45	Ser Ser Phe Glu Ser Thr Ile Glu Ile Phe His Ile Glu Ser Ser Gln		
	370	375	380

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Pro Ile His Thr Ile Glu Cys Gly Val Ser Ser Leu Met Trp His Pro
385 390 395 400

Thr Leu Pro Leu Leu Ala Tyr Ala Pro Glu Ser Ile Asn Glu Asn Asn
5 405 410 415

Lys Asp Pro Ser Ile Arg Val Phe Gly Tyr His Ser
420 425

10 (2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 517 amino acids
(B) TYPE: amino acid
15 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

20

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

25

(C) INDIVIDUAL ISOLATE: BETA TRCP, Fig. 13

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

Met Glu Gly Phe Ser Cys Ser Leu Gln Pro Pro Thr Ala Ser Glu Arg
30 1 5 10 15

Glu Asp Cys Asn Arg Asp Glu Pro Pro Arg Lys Ile Ile Thr Glu Lys
20 25 30

Asn Thr Leu Arg Gln Thr Lys Leu Ala Asn Gly Thr Ser Ser Met Ile
35 35 40 45

Val Pro Lys Gln Arg Lys Leu Ser Ala Asn Tyr Glu Lys Glu Lys Glu
50 55 60

40

Leu Cys Val Lys Tyr Phe Glu Gln Trp Ser Glu Cys Asp Gln Val Glu
65 70 75 80

Phe Val Glu His Leu Ile Ser Arg Met Cys His Tyr Gln His Gly His
45 85 90 95

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	Ile Asn Thr Tyr Leu Lys Pro Met Leu Gln Arg Asp Phe Ile Thr Ala	
	100	105 110
5	Leu Pro Ala Arg Gly Leu Asp His Ile Ala Glu Asn Ile Leu Ser Tyr	
	115	120 125
	Leu Asp Ala Lys Ser Leu Cys Ser Ala Glu Leu Val Cys Lys Glu Trp	
	130	135 140
10	Tyr Arg Val Thr Ser Asp Gly Met Leu Trp Lys Lys Leu Ile Glu Arg	
	145	150 155 160
	Met Val Arg Thr Asp Ser Leu Trp Arg Gly Leu Ala Glu Arg Arg Gly	
		165 170 175
15	Trp Gly Gln Tyr Leu Phe Lys Asn Lys Pro Pro Asp Gly Lys Thr Pro	
		180 185 190
	Pro Asn Ser Phe Tyr Arg Ala Leu Tyr Pro Lys Ile Ile Gln Asp Ile	
20		195 200 205
	Glu Thr Ile Glu Ser Asn Trp Arg Cys Gly Arg His Ser Leu Gln Arg	
	210	215 220
25	Ile His Cys Arg Ser Glu Thr Ser Lys Gly Val Tyr Cys Leu Gln Tyr	
	225	230 235 240
	Asp Asp Gln Lys Ile Val Ser Gly Leu Arg Asp Asn Thr Ile Lys Ile	
		245 250 255
30	Trp Asp Lys Asn Thr Leu Glu Cys Lys Arg Val Leu Met Gly His Thr	
	260	265 270
	Gly Ser Val Leu Cys Leu Gln Tyr Asp Glu Arg Val Ile Ile Thr Gly	
35		275 280 285
	Ser Asp Ser Thr Val Arg Val Trp Asp Val Asn Thr Gly Glu Met Leu	
	290	295 300
40	Asn Thr Leu Ile His His Cys Glu Ala Val Leu His Leu Arg Phe Asn	
	305	310 315 320
	Asn Gly Met Met Val Thr Cys Ser Lys Asp Arg Ser Ile Ala Val Trp	
		325 330 335
45	Asp Met Ala Ser Ala Thr Asp Ile Thr Leu Arg Arg Val Leu Val Gly	

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	Ile Asn Thr Tyr Leu Lys Pro Met Leu Gln Arg Asp Phe Ile Thr Ala
	100 105 110
5	Leu Pro Ala Arg Gly Leu Asp His Ile Ala Glu Asn Ile Leu Ser Tyr
	115 120 125
	Leu Asp Ala Lys Ser Leu Cys Ser Ala Glu Leu Val Cys Lys Glu Trp
	130 135 140
10	Tyr Arg Val Thr Ser Asp Gly Met Leu Trp Lys Lys Leu Ile Glu Arg
	145 150 155 160
	Met Val Arg Thr Asp Ser Leu Trp Arg Gly Leu Ala Glu Arg Arg Gly
	165 170 175
15	Trp Gly Gln Tyr Leu Phe Lys Asn Lys Pro Pro Asp Gly Lys Thr Pro
	180 185 190
	Pro Asn Ser Phe Tyr Arg Ala Leu Tyr Pro Lys Ile Ile Gln Asp Ile
20	195 200 205
	Glu Thr Ile Glu Ser Asn Trp Arg Cys Gly Arg His Ser Leu Gln Arg
	210 215 220
25	Ile His Cys Arg Ser Glu Thr Ser Lys Gly Val Tyr Cys Leu Gln Tyr
	225 230 235 240
	Asp Asp Gln Lys Ile Val Ser Gly Leu Arg Asp Asn Thr Ile Lys Ile
	245 250 255
30	Trp Asp Lys Asn Thr Leu Glu Cys Lys Arg Val Leu Met Gly His Thr
	260 265 270
	Gly Ser Val Leu Cys Leu Gln Tyr Asp Glu Arg Val Ile Ile Thr Gly
35	275 280 285
	Ser Asp Ser Thr Val Arg Val Trp Asp Val Asn Thr Gly Glu Met Leu
	290 295 300
40	Asn Thr Leu Ile His His Cys Glu Ala Val Leu His Leu Arg Phe Asn
	305 310 315 320
	Asn Gly Met Met Val Thr Cys Ser Lys Asp Arg Ser Ile Ala Val Trp
	325 330 335
45	Asp Met Ala Ser Ala Thr Asp Ile Thr Leu Arg Arg Val Leu Val Gly

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	340	345	350
	His Arg Ala Ala Val Asn Val Val Asp Phe Asp Asp Lys Tyr Ile Val		
	355	360	365
5	Ser Ala Ser Gly Asp Arg Thr Ile Lys Val Trp Asn Thr Ser Thr Cys		
	370	375	380
	Glu Phe Val Arg Thr Leu Asn Gly His Lys Arg Gly Ile Ala Cys Leu		
10	385	390	395 400
	Gln Tyr Arg Asp Arg Leu Val Val Ser Gly Ser Ser Asp Asn Thr Ile		
	405	410	415
15	Arg Leu Trp Asp Ile Glu Cys Gly Ala Cys Leu Arg Val Leu Glu Gly		
	420	425	430
	His Glu Glu Leu Val Arg Cys Ile Arg Phe Asp Asn Lys Arg Ile Val		
	435	440	445
20	Ser Gly Ala Tyr Asp Gly Lys Ile Lys Val Trp Asp Leu Val Ala Ala		
	450	455	460
	Leu Asp Pro Arg Ala Pro Ala Gly Thr Leu Cys Leu Arg Thr Leu Val		
25	465	470	475 480
	Glu His Ser Gly Arg Val Phe Arg Leu Gln Phe Asp Glu Phe Gln Ile		
	485	490	495
30	Val Ser Ser Ser His Asp Asp Thr Ile Leu Ile Trp Asp Phe Leu Asn		
	500	505	510
	Asp Pro Gly Leu Ala		
	515		

35

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

40

(A) LENGTH: 906 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

45

(iii) HYPOTHETICAL: NO

- 83 -

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: beta-prime-cop, Fig. 14

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

10	Met	Pro	Leu	Arg	Leu	Asp	Ile	Lys	Arg	Lys	Leu	Thr	Ala	Arg	Ser	Asp
	1				5					10					15	
	Arg	Val	Lys	Ser	Val	Asp	Leu	His	Pro	Thr	Glu	Pro	Trp	Met	Leu	Ala
					20				25					30		
15	Ser	Leu	Tyr	Asn	Gly	Ser	Val	Cys	Val	Trp	Asn	His	Glu	Thr	Gln	Thr
			35					40					45			
	Leu	Val	Lys	Thr	Phe	Glu	Val	Cys	Asp	Leu	Pro	Val	Arg	Ala	Ala	Lys
		50					55					60				
20	Phe	Val	Ala	Arg	Lys	Asn	Trp	Val	Val	Thr	Gly	Ala	Asp	Asp	Met	Gln
	65					70				75					80	
	Ile	Arg	Val	Phe	Asn	Tyr	Asn	Thr	Leu	Glu	Arg	Val	His	Met	Phe	Glu
25					85				90					95		
	Ala	His	Ser	Asp	Tyr	Ile	Arg	Cys	Ile	Ala	Val	His	Pro	Thr	Gln	Pro
				100					105					110		
30	Phe	Ile	Leu	Thr	Ser	Ser	Asp	Asp	Met	Leu	Ile	Lys	Leu	Trp	Asp	Trp
			115					120					125			
	Asp	Lys	Lys	Trp	Ser	Cys	Ser	Gln	Val	Phe	Glu	Gly	His	Thr	His	Tyr
		130					135				140					
35	Val	Met	Gln	Ile	Val	Ile	Asn	Pro	Lys	Asp	Asn	Asn	Gln	Phe	Ala	Ser
	145					150					155				160	
	Ala	Ser	Leu	Asp	Arg	Thr	Ile	Lys	Val	Trp	Gln	Leu	Gly	Ser	Ser	Ser
40					165					170					175	
	Pro	Asn	Phe	Thr	Leu	Glu	Gly	His	Glu	Lys	Gly	Val	Asn	Cys	Ile	Asp
				180					185				190			
45	Tyr	Tyr	Ser	Gly	Gly	Asp	Lys	Pro	Tyr	Leu	Ile	Ser	Gly	Ala	Asp	Asp
				195				200					205			

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	Arg	Leu	Val	Lys	Ile	Trp	Asp	Tyr	Gln	Asn	Lys	Thr	Cys	Val	Gln	Thr	
	210						215					220					
5	Leu	Glu	Gly	His	Ala	Gln	Asn	Val	Ser	Cys	Ala	Ser	Phe	His	Pro	Glu	
	225					230					235					240	
	Leu	Pro	Ile	Ile	Ile	Thr	Gly	Ser	Glu	Asp	Gly	Thr	Val	Arg	Ile	Trp	
					245					250					255		
10	His	Ser	Ser	Thr	Tyr	Arg	Leu	Glu	Ser	Thr	Leu	Asn	Tyr	Gly	Met	Glu	
				260					265					270			
	Arg	Val	Trp	Cys	Val	Ala	Ser	Leu	Arg	Gly	Ser	Asn	Asn	Val	Ala	Leu	
				275				280					285				
15	Gly	Tyr	Asp	Glu	Gly	Ser	Ile	Ile	Val	Lys	Leu	Gly	Arg	Glu	Glu	Pro	
	290					295					300						
	Ala	Met	Ser	Met	Asp	Ala	Asn	Gly	Lys	Ile	Ile	Trp	Ala	Lys	His	Ser	
20	305					310					315					320	
	Glu	Val	Gln	Gln	Ala	Asn	Leu	Lys	Ala	Met	Gly	Asp	Ala	Glu	Ile	Lys	
				325					330					335			
25	Asp	Gly	Glu	Arg	Leu	Pro	Leu	Ala	Val	Lys	Asp	Met	Gly	Ser	Cys	Glu	
				340				345					350				
	Ile	Tyr	Pro	Gln	Thr	Ile	Gln	His	Asn	Pro	Asn	Gly	Arg	Phe	Val	Val	
				355				360					365				
30	Val	Cys	Gly	Asp	Gly	Glu	Tyr	Ile	Ile	Tyr	Thr	Ala	Met	Ala	Leu	Arg	
				370				375				380					
	Asn	Lys	Ser	Phe	Gly	Ser	Ala	Gln	Glu	Phe	Ala	Trp	Ala	His	Asp	Ser	
35	385					390					395					400	
	Ser	Glu	Tyr	Ala	Ile	Arg	Glu	Ser	Asn	Ser	Val	Val	Lys	Ile	Phe	Lys	
				405					410					415			
40	Asn	Phe	Lys	Glu	Lys	Lys	Ser	Phe	Lys	Pro	Asp	Phe	Gly	Ala	Glu	Ser	
				420					425					430			
	Ile	Tyr	Gly	Gly	Phe	Leu	Leu	Gly	Val	Arg	Ser	Val	Asn	Gly	Leu	Ala	
				435				440					445				
45	Phe	Tyr	Asp	Trp	Glu	Asn	Thr	Glu	Leu	Ile	Arg	Arg	Ile	Glu	Ile	Gln	

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	450	455	460
	Pro Lys His Ile Phe Trp Ser Asp Ser Gly Glu Leu Val Cys Ile Ala		
	465	470	475 480
5	Thr Glu Glu Ser Phe Phe Ile Leu Lys Tyr Leu Ser Glu Lys Val Leu		
	485	490	495
	Ala Ala Gln Glu Thr His Glu Gly Val Thr Glu Asp Gly Ile Glu Asp		
10	500	505	510
	Gly Phe Glu Val Leu Gly Glu Ile Gln Glu Ile Val Lys Thr Gly Leu		
	515	520	525
15	Trp Val Gly Asp Cys Phe Ile Tyr Thr Ser Ser Val Asn Arg Leu Asn		
	530	535	540
	Tyr Tyr Val Gly Gly Glu Ile Val Thr Ile Ala His Leu Asp Arg Thr		
	545	550	555 560
20	Met Tyr Leu Leu Gly Tyr Ile Pro Lys Asp Asn Arg Leu Tyr Leu Gly		
	565	570	575
	Asp Lys Glu Leu Asn Ile Val Ser Tyr Ser Leu Leu Val Ser Val Leu		
25	580	585	590
	Glu Tyr Gln Thr Ala Val Met Arg Arg Asp Phe Ser Met Ala Asp Lys		
	595	600	605
30	Val Leu Pro Thr Ile Pro Lys Glu Gln Arg Thr Arg Val Ala His Phe		
	610	615	620
	Leu Glu Lys Gln Gly Phe Lys Gln Gln Ala Leu Thr Val Ser Thr Asp		
	625	630	635 640
35	Pro Glu His Arg Phe Glu Leu Ala Leu Gln Leu Gly Glu Leu Lys Ile		
	645	650	655
	Ala Tyr Gln Leu Ala Val Glu Ala Glu Ser Glu Gln Lys Trp Lys Gln		
40	660	665	670
	Leu Ala Glu Leu Ala Ile Ser Lys Cys Pro Phe Gly Leu Ala Gln Glu		
	675	680	685
45	Cys Leu His His Ala Gln Asp Tyr Gly Gly Leu Leu Leu Leu Ala Thr		
	690	695	700

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	Ala Ser Gly Asn Ala Ser Met Val Asn Lys Leu Ala Glu Gly Ala Glu,	
	705	710 715 720
5	Arg Asp Gly Lys Asn Asn Val Ala Phe Met Ser Tyr Phe Leu Gln Gly	
		725 730 735
	Lys Leu Asp Ala Cys Leu Glu Leu Leu Ile Arg Thr Gly Arg Leu Pro	
		740 745 750
10	Glu Ala Ala Phe Leu Ala Arg Thr Tyr Leu Pro Ser Gln Val Ser Arg	
		755 760 765
	Val Val Lys Leu Trp Arg Glu Asn Leu Ser Lys Val Asn Gln Lys Ala	
		770 775 780
15	Ala Glu Ser Leu Ala Asp Pro Thr Glu Tyr Glu Asn Leu Phe Pro Gly	
		785 790 795 800
	Leu Lys Glu Ala Phe Val Val Glu Glu Trp Val Lys Glu Thr His Ala	
20		805 810 815
	Asp Leu Trp Pro Ala Lys Gln Tyr Pro Leu Val Thr Pro Asn Glu Glu	
		820 825 830
25	Arg Asn Val Met Glu Glu Ala Lys Gly Phe Gln Pro Ser Arg Ser Ala	
		835 840 845
	Ala Gln Gln Glu Leu Asp Gly Lys Pro Ala Ser Pro Thr Pro Val Ile	
		850 855 860
30	Val Thr Ser Gln Thr Ala Asn Lys Glu Glu Lys Ser Leu Leu Glu Leu	
		865 870 875 880
	Glu Val Asp Leu Asp Asn Leu Glu Ile Glu Asp Ile Asp Thr Thr Asp	
35		885 890 895
	Ile Asn Leu Asp Glu Asp Ile Leu Asp Asp	
		900 905

40 (2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 779 amino acids

(B) TYPE: amino acid

45 (D) TOPOLOGY: unknown

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(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

5 (iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(c) INDIVIDUAL ISOLATE: CDC4 / CDC20 protein, Fig. 15

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Met Gly Ser Phe Pro Leu Ala Glu Phe Pro Leu Arg Asp Ile Pro Val
 1 5 10 15
 Pro Tyr Ser Tyr Arg Val Ser Gly Gly Ile Ala Ser Ser Gly Ser Val
 20 25 30
 Thr Ala Leu Val Thr Ala Ala Gly Thr His Arg Asn Ser Ser Thr Ala
 20 35 40 45
 Lys Thr Val Glu Thr Glu Asp Gly Glu Glu Asp Ile Asp Glu Tyr Gln
 50 55 60
 Arg Lys Arg Ala Ala Gly Ser Gly Glu Ser Thr Pro Glu Arg Ser Asp
 25 65 70 75 80
 Phe Lys Arg Val Lys His Asp Asn His Lys Thr Leu His Pro Val Asn
 85 90 95
 30 Leu Gln Asn Thr Gly Ala Ala Ser Val Asp Asn Asp Gly Leu His Asn
 100 105 110
 Leu Thr Asp Ile Ser Asn Asp Ala Glu Lys Leu Leu Met Ser Val Asp
 35 115 120 125
 Asp Gly Ser Ala Ala Pro Ser Thr Leu Ser Val Asn Met Gly Val Ala
 130 135 140
 40 Ser His Asn Val Ala Ala Pro Thr Thr Val Asn Ala Ala Thr Ile Thr
 145 150 155 160
 Gly Ser Asp Val Ser Asn Asn Val Asn Ser Ala Thr Ile Asn Asn Pro
 165 170 175
 45 Met Glu Glu Gly Ala Leu Pro Leu Ser Pro Thr Ala Ser Ser Pro Gly

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	180	185	190
	Thr Thr Thr Pro Leu Ala Lys Thr Thr Lys Thr Ile Asn Asn Asn Asn		
	195	200	205
5	Asn Ile Ala Asp Leu Ile Glu Ser Lys Asp Ser Ile Ile Ser Pro Glu		
	210	215	220
	Tyr Leu Ser Asp Glu Ile Phe Ser Ala Ile Asn Asn Asn Leu Pro His		
10	225	230	235 240
	Ala Tyr Phe Lys Asn Leu Leu Phe Arg Leu Val Ala Asn Met Asp Arg		
	245	250	255
15	Ser Glu Leu Ser Asp Leu Gly Thr Leu Ile Lys Asp Asn Leu Lys Arg		
	260	265	270
	Asp Leu Ile Thr Ser Leu Pro Phe Glu Ile Ser Leu Lys Ile Phe Asn		
	275	280	285
20	Tyr Leu Gln Phe Glu Asp Ile Ile Asn Ser Leu Gly Val Ser Gln Asn		
	290	295	300
	Trp Asn Lys Ile Ile Arg Lys Ser Thr Ser Leu Trp Lys Lys Leu Leu		
25	305	310	315 320
	Ile Ser Glu Asn Phe Val Ser Pro Lys Gly Phe Asn Ser Leu Asn Leu		
	325	330	335
30	Lys Leu Ser Gln Lys Tyr Pro Lys Leu Ser Gln Gln Asp Arg Leu Arg		
	340	345	350
	Leu Ser Phe Leu Glu Asn Ile Phe Ile Leu Lys Asn Trp Tyr Asn Pro		
	355	360	365
35	Lys Phe Val Pro Gln Arg Thr Thr Leu Arg Gly His Met Thr Ser Val		
	370	375	380
	Ile Thr Cys Leu Gln Phe Glu Asp Asn Tyr Val Ile Thr Gly Ala Asp		
40	385	390	395 400
	Asp Lys Met Ile Arg Val Tyr Asp Ser Ile Asn Lys Lys Phe Leu Leu		
	405	410	415
45	Gln Leu Ser Gly His Asp Gly Gly Val Trp Ala Leu Lys Tyr Ala His		
	420	425	430

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	Gly Gly Ile Leu Val Ser Gly Ser Thr Asp Arg Thr Val Arg Val Trp
	435 440 445
5	Asp Ile Lys Lys Gly Cys Cys Thr His Val Phe Glu Gly His Asn Ser
	450 455 460
	Thr Val Arg Cys Leu Asp Ile Val Glu Tyr Lys Asn Ile Lys Tyr Ile
	465 470 475 480
10	Val Thr Gly Ser Arg Asp Asn Thr Leu His Val Trp Lys Leu Pro Lys
	485 490 495
	Glu Ser Ser Val Pro Asp His Gly Glu Glu His Asp Tyr Pro Leu Val
	500 505 510
15	Phe His Thr Pro Glu Glu Asn Pro Tyr Phe Val Gly Val Leu Arg Gly
	515 520 525
	His Met Ala Ser Val Arg Thr Val Ser Gly His Gly Asn Ile Val Val
20	530 535 540
	Ser Gly Ser Tyr Asp Asn Thr Leu Ile Val Trp Asp Val Ala Gln Met
	545 550 555 560
25	Lys Cys Leu Tyr Ile Leu Ser Gly His Thr Asp Arg Ile Tyr Ser Thr
	565 570 575
	Ile Tyr Asp His Glu Arg Lys Arg Cys Ile Ser Ala Ser Met Asp Thr
	580 585 590
30	Thr Ile Arg Ile Trp Asp Leu Glu Asn Ile Trp Asn Asn Gly Glu Cys
	595 600 605
	Ser Tyr Ala Thr Asn Ser Ala Ser Pro Cys Ala Lys Ile Leu Gly Ala
35	610 615 620
	Met Tyr Thr Leu Gln Gly His Thr Ala Leu Val Gly Leu Leu Arg Leu
	625 630 635 640
40	Ser Asp Lys Phe Leu Val Ser Ala Ala Ala Asp Gly Ser Ile Arg Gly
	645 650 655
	Trp Asp Ala Asn Asp Tyr Ser Arg Lys Phe Ser Tyr His His Thr Asn
	660 665 670
45	Leu Ser Ala Ile Thr Thr Phe Tyr Val Ser Asp Asn Ile Leu Val Ser

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675 680 685
 Gly Ser Glu Asn Gln Phe Asn Ile Tyr Asn Leu Arg Ser Gly Lys Leu
 690 695 700
 5
 Val His Ala Asn Ile Leu Lys Asp Ala Asp Gln Ile Trp Ser Val Asn
 705 710 715 720
 Phe Lys Gly Lys Thr Leu Val Ala Ala Val Glu Lys Asp Gly Gln Ser
 10 725 730 735
 Phe Leu Glu Ile Leu Asp Phe Ser Lys Ala Ser Lys Ile Asn Tyr Val
 740 745 750
 15 Ser Asn Pro Val Asn Ser Ser Ser Ser Ser Leu Glu Ser Ile Ser Thr
 755 760 765
 Ser Leu Gly Leu Thr Arg Thr Thr Ile Ile Pro
 770 775
 20
 (2) INFORMATION FOR SEQ ID NO:33:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 318 amino acids
 25 (B) TYPE: amino acid
 (D) TOPOLOGY: unknown
 (ii) MOLECULE TYPE: protein
 30 (iii) HYPOTHETICAL: NO
 (iv) ANTI-SENSE: NO
 (vi) ORIGINAL SOURCE:
 35 (C) INDIVIDUAL ISOLATE: GBLP -CHLAMIDOMONAS HOMOLOG, Fig. 16
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:
 40 Met Ala Glu Thr Leu Thr Leu Arg Ala Thr Leu Lys Gly His Thr Asn
 1 5 10 15
 Trp Val Thr Ala Ile Ala Thr Pro Leu Asp Pro Ser Ser Asn Thr Leu
 20 25 30
 45 Leu Ser Ala Ser Arg Asp Lys Ser Val Leu Val Trp Glu Leu Glu Arg

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	35	40	45
	Ser Glu Ser Asn Tyr Gly Tyr Ala Arg Lys Ala Leu Arg Gly His Ser		
	50	55	60
5	His Phe Val Gln Asp Val Val Ile Ser Ser Asp Gly Gln Phe Cys Leu		
	65	70	75 80
	Thr Gly Ser Trp Asp Gly Thr Leu Arg Leu Trp Asp Leu Asn Thr Gly		
10		85	90 95
	Thr Thr Thr Arg Arg Phe Val Gly His Thr Lys Asp Val Leu Ser Val		
		100	105 110
15	Ala Phe Ser Val Asp Asn Arg Gln Ile Val Ser Gly Ser Arg Asp Lys		
		115	120 125
	Thr Ile Lys Leu Trp Asn Thr Leu Gly Glu Cys Lys Tyr Thr Ile Gly		
		130	135 140
20	Glu Pro Glu Gly His Thr Glu Trp Val Ser Cys Val Arg Phe Ser Pro		
		145	150 155 160
	Met Thr Thr Asn Pro Ile Ile Val Ser Gly Gly Trp Asp Lys Met Val		
25		165	170 175
	Lys Val Trp Asn Leu Thr Asn Cys Lys Leu Lys Asn Asn Leu Val Gly		
		180	185 190
30	His His Gly Tyr Val Asn Thr Val Thr Val Ser Pro Asp Gly Ser Leu		
		195	200 205
	Cys Ala Ser Gly Gly Lys Asp Gly Ile Ala Met Leu Trp Asp Leu Ala		
		210	215 220
35	Glu Gly Lys Arg Leu Tyr Ser Leu Asp Ala Gly Asp Val Ile His Cys		
		225	230 235 240
	Leu Cys Phe Ser Pro Asn Arg Tyr Trp Leu Cys Ala Ala Thr Gln Ser		
40		245	250 255
	Ser Ile Lys Ile Trp Asp Leu Glu Ser Lys Ser Ile Val Asp Asp Leu		
		260	265 270
45	Arg Pro Glu Phe Asn Ile Thr Ser Lys Lys Ala Gln Val Pro Tyr Cys		
		275	280 285

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Val Ser Leu Ala Trp Ser Ala Asp Gly Ser Thr Leu Tyr Ser Gly Tyr
 290 295 300

Thr Asp Gly Gln Ile Arg Val Trp Ala Val Gly His Ser Leu
 5 305 310 315

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 658 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

15

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

20

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: cop-1 protein, Fig. 17

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

25

Met Glu Glu Ile Ser Thr Asp Pro Val Val Pro Ala Val Lys Pro Asp
 1 5 10 15

30

Pro Arg Thr Ser Ser Val Gly Glu Gly Ala Asn Arg His Glu Asn Asp
 20 25 30

Asp Gly Gly Ser Gly Gly Ser Glu Ile Gly Ala Pro Asp Leu Asp Lys
 35 40 45

35

Asp Leu Leu Cys Pro Ile Cys Met Gln Ile Ile Lys Asp Ala Phe Leu
 50 55 60

40

Thr Ala Cys Gly His Ser Phe Cys Tyr Met Cys Ile Ile Thr His Leu
 65 70 75 80

Arg Asn Lys Ser Asp Cys Pro Cys Cys Ser Gln His Leu Thr Asn Asn
 85 90 95

45

Gln Leu Tyr Pro Asn Phe Leu Leu Asp Lys Leu Leu Lys Lys Thr Ser
 100 105 110

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	Ala Arg His Val Ser Lys Thr	Ala Ser Pro Leu Asp	Gln Phe Arg Glu
	115	120	125
5	Ala Leu Gln Arg Gly Cys Asp Val Ser Ile Lys	Glu Val Asp Asn Leu	
	130	135	140
	Leu Thr Leu Leu Ala Glu Arg Lys Arg Lys Met	Glu Gln Glu Glu Ala	
	145	150	155 160
10	Glu Arg Asn Met Gln Ile Leu Leu Asp Phe Leu His	Cys Leu Arg Lys	
	165	170	175
	Gln Lys Val Asp Glu Leu Asn Glu Val Gln Thr Asp	Leu Gln Tyr Ile	
	180	185	190
15	Lys Glu Asp Ile Asn Ala Val Glu Arg His Arg Ile	Asp Leu Tyr Arg	
	195	200	205
	Ala Arg Asp Arg Tyr Ser Val Lys Leu Arg Met	Leu Gly Asp Asp Pro	
20	210	215	220
	Ser Thr Arg Asn Ala Trp Pro His Glu Lys Asn Gln Ile Gly	Phe Asn	
	225	230	235 240
25	Ser Asn Ser Leu Ser Ile Arg Gly Gly Asn Phe Val Gly	Asn Tyr Gln	
	245	250	255
	Asn Lys Lys Val Glu Gly Lys Ala Gln Gly Ser Ser His Gly	Leu Pro	
	260	265	270
30	Lys Lys Asp Ala Leu Ser Gly Ser Asp Ser Gln Ser	Leu Asn Gln Ser	
	275	280	285
	Thr Val Ser Met Ala Arg Lys Lys Arg Ile His Ala Gln Phe	Asn Asp	
35	290	295	300
	Leu Gln Glu Cys Tyr Leu Gln Lys Arg Arg Gln Leu Ala Asp	Gln Pro	
	305	310	315 320
40	Asn Ser Lys Gln Glu Asn Asp Lys Ser Val Val Arg Arg	Glu Gly Tyr	
	325	330	335
	Ser Asn Gly Leu Ala Asp Phe Gln Ser Val Leu Thr Thr Phe Thr	Arg	
	340	345	350
45	Tyr Ser Arg Leu Arg Val Ile Ala Glu Ile Arg His Gly Asp	Ile Phe	

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	355		360		365
	His Ser Ala Asn Ile Val	Ser Ser Ile Glu Phe	Asp Arg Asp Asp Glu		
	370	375	380		
5	Leu Phe Ala Thr Ala Gly Val	Ser Arg Cys Ile Lys Val	Phe Asp Phe		
	385	390	395	400	
	Ser Ser Val Val Asn Glu Pro	Ala Asp Met Gln Cys Pro	Ile Val Glu		
10		405	410	415	
	Met Ser Thr Arg Ser Lys Leu	Ser Cys Leu Ser Trp Asn	Lys His Glu		
		420	425	430	
15	Lys Asn His Ile Ala Ser Ser	Asp Tyr Glu Gly Ile Val	Thr Val Trp		
		435	440	445	
	Asp Val Thr Thr Arg Gln Ser	Leu Met Glu Thr Glu Glu	Asn Glu Lys		
		450	455	460	
20	Arg Ala Trp Ser Val Asp Phe	Ser Arg Thr Glu Pro Ser	Met Leu Val		
		465	470	475	480
	Ser Gly Ser Asp Asp Cys Lys	Val Lys Val Trp Cys Thr	Arg Gln Glu		
25		485	490	495	
	Ala Ser Val Ile Asn Ile Asp	Met Lys Ala Asn Ile Cys	Cys Val Lys		
		500	505	510	
30	Tyr Asn Pro Gly Ser Ser Asn	Tyr Ile Ala Val Gly Ser	Ala Asp His		
		515	520	525	
	His Ile His Tyr Tyr Asp Leu	Arg Asn Ile Ser Gln Pro	Leu His Val		
		530	535	540	
35	Phe Ser Gly His Lys Lys Ala	Val Ser Tyr Met Lys Phe	Leu Ser Asn		
		545	550	555	560
	Asn Glu Leu Ala Ser Ala Ser	Thr Asp Ser Thr Leu Arg	Leu Trp Asp		
40		565	570	575	
	Val Lys Asp Asn Leu Pro Val	Arg Thr Phe Arg Gly His	Thr Asn Glu		
		580	585	590	
45	Lys Asn Phe Val Gly Leu Thr	Val Asn Ser Glu Tyr Leu	Ala Cys Gly		
		595	600	605	

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Ser Glu Thr Thr Arg Tyr Val Tyr His Lys Glu Ile Thr Arg Pro Val
610 615 620

Thr Ser His Arg Phe Gly Ser Pro Asp Met Asp Asp Ala Glu Lys Arg
5 625 630 635 640

Gln Val Pro Thr Leu Leu Val Arg Phe Ala Gly Arg Val Ile Val Pro
645 650 655

10 Arg Cys

(2) INFORMATION FOR SEQ ID NO:35:

15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 440 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: unknown

20 (ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

25

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: CORO PROTEIN, Fig. 18

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

Met Ser Lys Val Val Arg Ser Ser Lys Tyr Arg His Val Phe Ala Ala
1 5 10 15

Gln Pro Lys Lys Glu Glu Cys Tyr Gln Asn Leu Lys Thr Lys Ser Ala
20 25 30

Val Trp Asp Ser Asn Tyr Val Ala Ala Asn Thr Arg Tyr Ile Trp Asp
35 40 45

Ala Ala Gly Gly Gly Ser Phe Ala Val Glu Ala Ile Pro His Ser Gly
50 55 60

Lys Thr Thr Ser Val Pro Leu Phe Asn Gly His Lys Ser Ala Val Leu
45 65 70 75 80

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	Asp	Ile	Ala	Phe	His	Pro	Phe	Asn	Glu	Asn	Leu	Val	Gly	Ser	Val	Ser			
						85					90					95			
5	Glu	Asp	Cys	Asn	Ile	Cys	Ile	Trp	Gly	Ile	Pro	Glu	Gly	Gly	Leu	Thr			
				100					105					110					
	Asp	Ser	Ile	Ser	Thr	Pro	Leu	Gln	Thr	Leu	Ser	Gly	His	Lys	Arg	Lys			
				115				120					125						
10	Val	Gly	Thr	Ile	Ser	Phe	Gly	Pro	Val	Ala	Asp	Asn	Val	Ala	Val	Thr			
		130					135					140							
	Ser	Ser	Gly	Asp	Phe	Leu	Val	Lys	Thr	Trp	Asp	Val	Glu	Gln	Gly	Lys			
	145					150					155					160			
15	Asn	Leu	Thr	Thr	Val	Glu	Gly	His	Ser	Asp	Met	Ile	Thr	Ser	Cys	Glu			
					165					170					175				
	His	Asn	Gly	Ser	Gln	Ile	Val	Thr	Thr	Cys	Lys	Asp	Lys	Lys	Ala	Arg			
20				180					185					190					
	Val	Phe	Asp	Pro	Arg	Thr	Asn	Ser	Ile	Val	Asn	Glu	Val	Val	Cys	His			
			195					200					205						
25	Gln	Gly	Val	Lys	Asn	Ser	Arg	Ala	Ile	Phe	Ala	Lys	Asp	Lys	Val	Ile			
		210					215					220							
	Thr	Val	Gly	Phe	Ser	Lys	Thr	Ser	Glu	Arg	Glu	Leu	His	Ile	Tyr	Asp			
	225					230					235					240			
30	Pro	Arg	Ala	Phe	Thr	Thr	Pro	Leu	Ser	Ala	Gln	Val	Val	Asp	Ser	Ala			
					245					250					255				
	Ser	Gly	Leu	Leu	Met	Pro	Phe	Tyr	Asp	Ala	Asp	Asn	Ser	Ile	Leu	Tyr			
35				260					265					270					
	Leu	Ala	Gly	Lys	Gly	Asp	Gly	Asn	Ile	Arg	Tyr	Tyr	Glu	Leu	Val	Asp			
		275					280						285						
40	Glu	Ser	Pro	Tyr	Ile	His	Phe	Leu	Ser	Glu	Phe	Lys	Ser	Ala	Thr	Pro			
		290					295					300							
	Gln	Arg	Gly	Leu	Cys	Phe	Leu	Pro	Lys	Arg	Cys	Leu	Asn	Thr	Ser	Glu			
	305					310					315					320			
45	Cys	Glu	Ile	Ala	Arg	Gly	Leu	Lys	Val	Thr	Pro	Phe	Thr	Val	Glu	Pro			

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[illegible]

(2) INFORMATION FOR SEQ ID NO:36:

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 445 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: unknown

30

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

35

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Coronin (p55), Fig. 19

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Met Ser Lys Val Val Arg Ser Ser Lys Tyr Arg His Val Phe Ala Ala
1 5 10 15
45
Gln Pro Lys Lys Glu Glu Cys Tyr Gln Asn Leu Lys Val Thr Lys Ser

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	20	25	30
	Ala Trp Asp Ser Asn Tyr Val	Ala Ala Asn Thr Arg Tyr Phe Gly Val	
	35	40	45
5	Ile Trp Asp Ala Ala Gly Gly Gly Ser Phe Ala Val Ile Pro His Glu		
	50	55	60
	Ala Ser Gly Lys Thr Thr Ser Val Pro Leu Phe Asn Gly His Lys Ser		
10	65	70	75 80
	Ala Val Leu Asp Ile Ala Phe His Pro Phe Asn Glu Asn Leu Val Gly		
	85	90	95
15	Ser Val Ser Glu Asp Cys Asn Ile Cys Ile Trp Gly Ile Pro Glu Gly		
	100	105	110
	Gly Leu Thr Asp Ser Ile Ser Thr Pro Leu Gln Thr Leu Ser Gly His		
	115	120	125
20	Lys Arg Lys Val Gly Thr Ile Ser Phe Gly Pro Val Ala Asp Asn Val		
	130	135	140
	Ala Val Thr Ser Ser Gly Asp Phe Leu Val Lys Thr Trp Asp Val Glu		
25	145	150	155 160
	Gln Gly Lys Asn Leu Thr Thr Val Glu Gly His Ser Asp Met Ile Thr		
	165	170	175
30	Ser Cys Glu Trp Asn His Asn Gly Ser Gln Ile Val Thr Thr Cys Lys		
	180	185	190
	Asp Lys Lys Ala Arg Val Phe Asp Pro Arg Thr Asn Ser Ile Val Asn		
	195	200	205
35	Glu Val Val Cys His Gln Gly Val Lys Asn Ser Arg Ala Ile Phe Ala		
	210	215	220
	Lys Asp Lys Val Ile Thr Val Gly Phe Ser Lys Thr Ser Glu Arg Glu		
40	225	230	235 240
	Leu His Ile Tyr Asp Pro Arg Ala Phe Thr Thr Pro Leu Ser Ala Gln		
	245	250	255
45	Val Val Asp Ser Ala Ser Gly Leu Leu Met Pro Phe Tyr Asp Ala Asp		
	260	265	270

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	Asn Ser Ile Leu Tyr Leu Ala Gly Lys Gly Asp Gly Asn Ile Arg Tyr	
	275	280 285
5	Tyr Glu Leu Val Asp Glu Ser Pro Tyr Ile His Phe Leu Ser Glu Phe	
	290	295 300
	Lys Ser Ala Thr Pro Gln Arg Gly Leu Cys Phe Leu Pro Lys Arg Cys	
	305	310 315 320
10	Leu Asn Thr Ser Glu Cys Glu Ile Ala Arg Gly Leu Lys Val Thr Pro	
	325	330 335
	Phe Thr Val Glu Pro Ile Ser Phe Arg Val Pro Arg Lys Ser Asp Ile	
	340	345 350
15	Phe Gln Gly Asp Ile Tyr Pro Asp Thr Tyr Ala Gly Glu Pro Ser Leu	
	355	360 365
	Thr Ala Glu Gln Trp Val Ser Gly Thr Asn Ala Glu Pro Lys Thr Val	
20	370	375 380
	Ser Leu Ala Gly Gly Phe Val Lys Lys Ala Ser Ala Val Glu Phe Lys	
	385	390 395 400
25	Pro Val Val Gln Val Gln Glu Gly Pro Lys Asn Glu Lys Glu Leu Arg	
	405	410 415
	Glu Glu Tyr Glu Lys Leu Lys Ile Arg Val Ala Tyr Leu Glu Ser Glu	
	420	425 430
30	Ile Val Lys Lys Asp Ala Lys Ile Lys Glu Leu Thr Asn	
	435	440 445

(2) INFORMATION FOR SEQ ID NO:37:

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 431 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: unknown

40

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

45

(iv) ANTI-SENSE: NO

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(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: CSTF 50kDa, Fig. 20

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

	Met	Tyr	Arg	Thr	Lys	Val	Gly	Leu	Lys	Asp	Arg	Gln	Gln	Leu	Tyr	Lys	
	1				5					10					15		
10	Leu	Ile	Ile	Ser	Gln	Leu	Leu	Tyr	Asp	Gly	Tyr	Ile	Ser	Ile	Ala	Asn	
				20					25					30			
	Gly	Leu	Ile	Asn	Glu	Ile	Lys	Pro	Gln	Ser	Val	Cys	Ala	Pro	Ser	Glu	
			35					40					45				
15	Gln	Leu	Leu	His	Leu	Ile	Lys	Leu	Gly	Met	Glu	Asn	Asp	Asp	Thr	Ala	
		50					55					60					
	Val	Gln	Tyr	Ala	Ile	Gly	Arg	Ser	Asp	Thr	Val	Ala	Pro	Gly	Thr	Gly	
20	65					70					75					80	
	Ile	Asp	Leu	Glu	Phe	Asp	Ala	Asp	Val	Gln	Thr	Met	Ser	Pro	Glu	Ala	
					85					90					95		
25	Ser	Glu	Tyr	Glu	Thr	Cys	Tyr	Val	Thr	Ser	His	Lys	Gly	Pro	Cys	Arg	
				100					105					110			
	Val	Ala	Thr	Tyr	Ser	Arg	Asp	Gly	Gln	Leu	Ile	Ala	Thr	Gly	Ser	Ala	
				115				120					125				
30	Asp	Ala	Ser	Ile	Lys	Ile	Leu	Asp	Thr	Glu	Arg	Met	Leu	Ala	Lys	Ser	
		130					135					140					
	Ala	Met	Pro	Ile	Glu	Val	Met	Met	Asn	Glu	Thr	Ala	Gln	Gln	Asn	Met	
35	145					150					155				160		
	Glu	Asn	His	Pro	Val	Ile	Arg	Thr	Leu	Tyr	Asp	His	Val	Asp	Glu	Val	
					165					170				175			
40	Thr	Cys	Leu	Ala	Phe	His	Pro	Thr	Glu	Gln	Ile	Leu	Ala	Ser	Gly	Ser	
				180					185					190			
	Arg	Asp	Tyr	Thr	Leu	Lys	Leu	Phe	Asp	Tyr	Ser	Lys	Pro	Ser	Ala	Lys	
				195			200					205					
45	Arg	Ala	Phe	Lys	Tyr	Ile	Gln	Glu	Ala	Glu	Met	Leu	Arg	Ser	Ile	Ser	

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	210	215	220
	Phe His Pro Ser Gly Asp	Phe Ile Leu Val	Gly Thr Gln His Pro Thr
	225	230	235 240
5	Leu Arg Leu Tyr Asp Ile Asn Thr	Phe Gln Cys Phe Val Ser Cys Asn	
	245	250	255
10	Pro Gln Asp Gln His Thr Asp Ala Ile Cys Ser Val Asn Tyr Asn Ser		
	260	265	270
	Ser Ala Asn Met Tyr Val Thr Gly Ser Lys Asp Gly Cys Ile Lys Leu		
	275	280	285
15	Trp Asp Gly Val Ser Asn Arg Cys Ile Thr Thr Phe Glu Lys Ala His		
	290	295	300
	Asp Gly Ala Glu Val Cys Ser Ala Ile Phe Ser Lys Asn Ser Lys Tyr		
	305	310	315 320
20	Ile Leu Ser Ser Gly Lys Asp Ser Val Ala Lys Leu Trp Glu Ile Ser		
	325	330	335
	Thr Gly Arg Thr Leu Val Arg Tyr Thr Gly Ala Gly Leu Ser Gly Arg		
25	340	345	350
	Gln Val His Arg Thr Gln Ala Val Phe Asn His Thr Glu Asp Tyr Val		
	355	360	365
30	Leu Leu Pro Asp Glu Arg Thr Ile Ser Leu Cys Cys Trp Asp Ser Arg		
	370	375	380
	Thr Ala Glu Arg Arg Asn Leu Leu Ser Leu Gly His Asn Asn Ile Val		
	385	390	395 400
35	Arg Cys Ile Val His Ser Pro Thr Asn Pro Gly Phe Met Thr Cys Ser		
	405	410	415
	Asp Asp Phe Arg Ala Arg Phe Trp Tyr Arg Arg Ser Thr Thr Asp		
40	420	425	430

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 340 amino acids
(B) TYPE: amino acid

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(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

5 (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

10 (C) INDIVIDUAL ISOLATE: G-Beta 1 bovine, Fig. 21

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

15 Met Ser Glu Leu Asp Gln Leu Arg Gln Glu Ala Glu Gln Leu Lys Asn
 1 5 10 15
 Gln Ile Arg Asp Ala Arg Lys Ala Cys Ala Asp Ala Thr Leu Ser Gln
 20 20 25 30
 Ile Thr Asn Asn Ile Asp Pro Val Gly Arg Ile Gln Met Arg Thr Arg
 35 40 45
 Arg Thr Leu Arg Gly His Leu Ala Lys Ile Tyr Ala Met His Trp Gly
 25 50 55 60
 Thr Asp Ser Arg Leu Leu Val Ser Ala Ser Gln Asp Gly Lys Leu Ile
 65 70 75 80
 Ile Trp Asp Ser Tyr Thr Thr Asn Lys Val His Ala Ile Pro Leu Arg
 30 85 90 95
 Ser Ser Trp Val Met Thr Cys Ala Tyr Ala Pro Ser Gly Asn Tyr Val
 100 105 110
 35 Ala Cys Gly Gly Leu Asp Asn Ile Cys Ser Ile Tyr Asn Leu Lys Thr
 115 120 125
 Arg Glu Gly Asn Val Arg Val Ser Arg Glu Leu Ala Gly His Thr Gly
 40 130 135 140
 Tyr Leu Ser Cys Cys Arg Phe Leu Asp Asp Asn Gln Ile Val Thr Ser
 145 150 155 160
 45 Ser Gly Asp Thr Thr Cys Ala Leu Trp Asp Ile Glu Thr Gly Gln Gln
 165 170 175

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	Thr	Thr	Thr	Phe	Thr	Gly	His	Thr	Gly	Asp	Val	Met	Ser	Leu	Ser	Leu
				180					185					190		
5	Ala	Pro	Asp	Thr	Arg	Leu	Phe	Val	Ser	Gly	Ala	Cys	Asp	Ala	Ser	Ala
			195					200					205			
	Lys	Leu	Trp	Asp	Val	Arg	Glu	Gly	Met	Cys	Arg	Gln	Thr	Phe	Thr	Gly
		210					215					220				
10	His	Glu	Ser	Asp	Ile	Asn	Ala	Ile	Cys	Phe	Phe	Pro	Asn	Gly	Asn	Ala
	225					230					235					240
	Phe	Ala	Thr	Gly	Ser	Asp	Asp	Ala	Thr	Cys	Arg	Leu	Phe	Asp	Leu	Arg
				245						250				255		
15	Ala	Asp	Gln	Glu	Leu	Met	Thr	Tyr	Ser	His	Asp	Asn	Ile	Ile	Cys	Gly
			260					265					270			
	Ile	Thr	Ser	Val	Ser	Phe	Ser	Lys	Ser	Gly	Arg	Leu	Leu	Leu	Ala	Gly
20		275						280					285			
	Tyr	Asp	Asp	Phe	Asn	Cys	Asn	Val	Trp	Asp	Ala	Leu	Lys	Ala	Asp	Arg
	290					295					300					
25	Ala	Gly	Val	Leu	Ala	Gly	His	Asp	Asn	Arg	Val	Ser	Cys	Leu	Gly	Val
	305					310				315					320	
	Thr	Asp	Asp	Gly	Met	Ala	Val	Ala	Thr	Gly	Ser	Trp	Asp	Ser	Phe	Leu
				325						330				335		
30	Lys	Ile	Trp	Asn												
				340												

(2) INFORMATION FOR SEQ ID NO:39:

35

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 326 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: unknown

40

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

45

(iv) ANTI-SENSE: NO

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(vi) ORIGINAL SOURCE:

(c) INDIVIDUAL ISOLATE: G-Beta- bovine (2), Fig. 22

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

	Arg	Asn	Gln	Ile	Arg	Asp	Ala	Arg	Lys	Ala	Cys	Gly	Asp	Ser	Thr	Leu	
	1				5				10						15		
10	Thr	Gln	Ile	Thr	Ala	Gly	Leu	Asp	Pro	Val	Gly	Arg	Ile	Gln	Met	Arg	
				20					25					30			
	Thr	Arg	Arg	Thr	Leu	Arg	Gly	His	Leu	Ala	Lys	Ile	Tyr	Ala	Met	His	
				35				40					45				
15	Trp	Gly	Thr	Asp	Ser	Arg	Leu	Leu	Val	Ser	Ala	Ser	Gln	Asp	Gly	Lys	
		50					55					60					
	Leu	Ile	Ile	Trp	Asp	Ser	Glu	Gly	Asn	Val	Arg	Tyr	Thr	Thr	Asn	Lys	
20	65					70					75				80		
	Val	His	Ala	Ile	Pro	Leu	Arg	Ser	Ser	Trp	Val	Met	Thr	Cys	Ala	Tyr	
					85					90				95			
25	Ala	Pro	Ser	Gly	Asn	Phe	Val	Ala	Cys	Gly	Gly	Leu	Asp	Asn	Ile	Cys	
				100					105					110			
	Ser	Ile	Tyr	Ser	Leu	Lys	Thr	Arg	Val	Ser	Arg	Glu	Leu	Pro	Gly	His	
			115					120					125				
30	Thr	Gly	Tyr	Leu	Ser	Cys	Cys	Arg	Phe	Leu	Asp	Asp	Asn	Gln	Ile	Ile	
		130					135					140					
	Thr	Ser	Ser	Gly	Asp	Thr	Thr	Cys	Ala	Leu	Trp	Asp	Ile	Glu	Thr	Gly	
35	145					150					155				160		
	Gln	Gln	Thr	Val	Gly	Phe	Ala	Gly	His	Ser	Gly	Asp	Val	Met	Ser	Leu	
					165					170				175			
40	Ser	Leu	Ala	Pro	Asp	Gly	Arg	Thr	Phe	Val	Ser	Gly	Ala	Cys	Asp	Ala	
				180					185					190			
	Ser	Ile	Lys	Leu	Trp	Asp	Val	Arg	Asp	Ser	Met	Cys	Arg	Gln	Thr	Phe	
			195				200					205					
45	Ile	Gly	His	Glu	Ser	Asp	Ile	Asn	Ala	Val	Ala	Phe	Phe	Pro	Asn	Gly	

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	210	215	220
	Tyr Ala Phe Thr Thr Gly Ser Asp Asp Ala Thr Cys Arg Leu Phe Asp		
	225	230	235 240
5	Leu Arg Ala Asp Gln Glu Leu Leu Met Tyr Ser His Asp Asn Ile Ile		
	245	250	255
	Cys Gly Ile Thr Ser Val Ala Phe Ser Arg Ser Gly Arg Leu Leu Leu		
10	260	265	270
	Ala Gly Tyr Asp Asp Phe Asn Cys Asn Ile Trp Asp Ala Met Lys Gly		
	275	280	285
15	Asp Arg Ala Gly Val Leu Ala Gly His Asp Asn Arg Val Ser Cys Leu		
	290	295	300
	Gly Val Thr Asp Asp Gly Met Ala Val Ala Thr Gly Ser Trp Asp Ser		
	305	310	315 320
20	Phe Leu Lys Ile Trp Asn		
	325		

(2) INFORMATION FOR SEQ ID NO:40:

25

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 340 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: unknown

30

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

35

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: G- BETA DROSOPH, Fig. 23

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

Met Asn Glu Leu Asp Ser Leu Arg Gln Glu Ala Glu Ser Leu Lys Asn
1 5 10 15

45

Ala Ile Arg Asp Ala Arg Lys Ala Ala Cys Asp Thr Ser Leu Leu Gln

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	20	25	30
	Ala Ala Thr Ser Leu Glu Pro Ile Gly Arg Ile Gln Met Arg Thr Arg		
	35	40	45
5	Arg Thr Leu Arg Gly His Leu Ala Lys Ile Tyr Ala Met His Trp Gly		
	50	55	60
	Asn Asp Ser Arg Asn Leu Val Ser Ala Ser Gln Asp Gly Lys Leu Ile		
10	65	70	75 80
	Val Trp Asp Ser His Thr Thr Asn Lys Val His Ala Ile Pro Leu Arg		
	85	90	95
15	Ser Ser Trp Val Met Thr Cys Ala Tyr Ala Pro Ser Gly Ser Tyr Val		
	100	105	110
	Ala Cys Gly Gly Leu Asp Asn Met Cys Ser Ile Tyr Asn Leu Lys Thr		
	115	120	125
20	Arg Glu Gly Asn Val Arg Val Ser Arg Glu Leu Pro Gly His Gly Gly		
	130	135	140
	Tyr Leu Ser Cys Cys Arg Phe Leu Asp Asp Asn Gln Ile Val Thr Ser		
25	145	150	155 160
	Ser Gly Asp Met Ser Cys Gly Leu Trp Asp Ile Glu Thr Gly Leu Gln		
	165	170	175
30	Val Thr Ser Phe Leu Gly His Thr Gly Asp Val Met Ala Leu Ser Leu		
	180	185	190
	Ala Pro Gln Cys Lys Thr Phe Val Ser Gly Ala Cys Asp Ala Ser Ala		
	195	200	205
35	Lys Leu Trp Asp Ile Arg Glu Gly Val Cys Lys Gln Thr Phe Pro Gly		
	210	215	220
	His Glu Ser Asp Ile Asn Ala Val Thr Phe Phe Pro Asn Gly Gln Ala		
40	225	230	235 240
	Phe Ala Thr Gly Ser Asp Asp Ala Thr Cys Arg Leu Phe Asp Ile Arg		
	245	250	255
45	Ala Asp Gln Glu Leu Ala Met Tyr Ser His Asp Asn Ile Ile Cys Gly		
	260	265	270

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Ile Thr Ser Val Ala Phe Ser Lys Ser Gly Arg Leu Leu Leu Ala Gly
 275 280 285

5 Tyr Asp Asp Phe Asn Cys Asn Val Trp Asp Thr Met Lys Ala Glu Arg
 290 295 300

Ser Gly Ile Leu Ala Gly His Asp Asn Arg Val Ser Cys Leu Gly Val
 305 310 315 320

10 Thr Glu Asn Gly Met Ala Val Ala Thr Gly Ser Trp Asp Ser Phe Leu
 325 330 335

Arg Val Trp Asn
 340

15

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 317 amino acids
 20 (B) TYPE: amino acid
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

25 (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 30 (C) INDIVIDUAL ISOLATE: G-BETA HUMAN, Fig. 24

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

35 Met Thr Glu Gln Met Thr Leu Arg Gly Thr Leu Lys Gly His Asn Gly
 1 5 10 15

Trp Val Thr Gln Ile Ala Thr Thr Pro Gln Phe Pro Asp Met Ile Leu
 20 25 30

40 Ser Ala Ser Arg Asp Lys Thr Ile Ile Met Trp Lys Leu Thr Arg Asp
 35 40 45

Glu Thr Asn Tyr Gly Ile Pro Gln Arg Ala Leu Arg Gly His Ser His
 45 50 55 60

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	Phe Val Ser Asp Val Val Ile Ser Ser Asp Gly Gln Phe Ala Leu Ser	
	65	80
		70
		75
5	Gly Ser Trp Asp Gly Thr Leu Arg Leu Trp Asp Leu Thr Thr Gly Thr	
		95
		85
		90
	Thr Thr Arg Arg Phe Val Gly His Thr Lys Asp Val Leu Ser Val Ala	
		110
		100
		105
10	Phe Ser Ser Asp Asn Arg Gln Ile Val Ser Gly Ser Arg Asp Lys Thr	
		125
		115
		120
	Ile Lys Leu Trp Asn Thr Leu Gly Val Cys Lys Tyr Thr Val Gln Asp	
		140
		130
		135
15	Glu Ser His Ser Glu Trp Val Ser Cys Val Arg Phe Ser Pro Asn Ser	
		160
		145
		150
		155
	Ser Asn Pro Ile Ile Val Ser Cys Gly Trp Asp Lys Leu Val Lys Val	
		175
		165
		170
20	Trp Asn Leu Ala Asn Cys Lys Leu Lys Thr Asn His Ile Gly His Thr	
		190
		180
		185
	Gly Tyr Leu Asn Thr Val Thr Val Ser Pro Asp Gly Ser Leu Cys Ala	
		205
		195
		200
	Ser Gly Gly Lys Asp Gly Gln Ala Met Leu Trp Asp Leu Asn Glu Gly	
		220
		210
		215
30	Lys His Leu Tyr Thr Leu Asp Gly Gly Asp Ile Ile Asn Ala Leu Cys	
		240
		225
		230
		235
	Phe Ser Pro Asn Arg Tyr Trp Leu Cys Ala Ala Thr Gly Pro Ser Ile	
		255
		245
		250
35	Lys Ile Trp Asp Leu Glu Gly Lys Ile Ile Val Asp Glu Leu Lys Gln	
		270
		260
		265
	Glu Val Ile Ser Thr Ser Ser Lys Ala Glu Pro Pro Gln Cys Thr Ser	
		285
		275
		280
40	Leu Ala Trp Ser Ala Asp Gly Gln Thr Leu Phe Ala Gly Tyr Thr Asp	
		300
		290
		295
45	Asn Leu Val Arg Val Trp Gln Val Thr Ile Gly Thr Arg	

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305

310

315

(2) INFORMATION FOR SEQ ID NO:42:

5 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 340 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: unknown

10 (ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

15

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: G-Beta 2 (Human), Fig. 25

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

Met Ser Glu Leu Glu Gln Leu Arg Gln Glu Ala Glu Gln Leu Arg Asn
 1 5 10 15

Gln Ile Arg Asp Ala Arg Lys Ala Cys Gly Asp Ser Thr Leu Thr Gln
 20 25 30

Ile Thr Ala Gly Leu Asp Pro Val Gly Arg Ile Gln Met Arg Thr Arg
 35 40 45

Arg Thr Leu Arg Gly His Leu Ala Lys Ile Tyr Ala Met His Trp Gly
 50 55 60

Thr Asp Ser Arg Leu Leu Val Ser Ala Ser Gln Asp Gly Lys Leu Ile
 65 70 75 80

Ile Trp Asp Ser Tyr Thr Thr Asn Lys Val His Ala Ile Pro Leu Arg
 85 90 95

Ser Ser Trp Val Met Thr Cys Ala Tyr Ala Pro Ser Gly Asn Phe Val
 100 105 110

Ala Cys Gly Gly Leu Asp Asn Ile Cys Ser Ile Tyr Ser Leu Lys Thr
 115 120 125

45

Arg Glu Gly Asn Val Arg Val Ser Arg Glu Leu Pro Gly His Thr Gly

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	130	135	140
	Tyr Leu Ser Cys Cys Arg Phe Leu Asp Asp Asn Gln Ile Ile Thr Ser		
	145	150	155 160
5	Ser Gly Asp Thr Thr Cys Ala Leu Trp Asp Ile Glu Thr Gly Gln Gln		
		165	170 175
	Thr Val Gly Phe Ala Gly His Ser Gly Asp Val Met Ser Leu Ser Leu		
10		180	185 190
	Ala Pro Asp Gly Arg Thr Phe Val Ser Gly Ala Cys Asp Ala Ser Ile		
		195	200 205
15	Lys Leu Trp Asp Val Arg Asp Ser Met Cys Arg Gln Thr Phe Ile Gly		
		210	215 220
	His Glu Ser Asp Ile Asn Ala Val Ala Phe Phe Pro Asn Gly Tyr Ala		
		225	230 235 240
20	Phe Thr Thr Gly Ser Asp Asp Ala Thr Cys Arg Leu Phe Asp Leu Arg		
		245	250 255
	Ala Asp Gln Glu Leu Leu Met Tyr Ser His Asp Asn Ile Ile Cys Gly		
25		260	265 270
	Ile Thr Ser Val Ala Phe Ser Arg Ser Gly Arg Leu Leu Leu Ala Gly		
		275	280 285
30	Tyr Asp Asp Phe Asn Cys Asn Ile Trp Asp Ala Met Lys Gly Asp Arg		
		290	295 300
	Ala Gly Val Leu Ala Gly His Asp Asn Arg Val Ser Cys Leu Gly Val		
		305	310 315 320
35	Thr Asp Asp Gly Met Ala Val Ala Thr Gly Ser Trp Asp Ser Phe Leu		
		325	330 335
	Lys Ile Trp Asn		
40		340	

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 29 amino acids
(B) TYPE: amino acid

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(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

5 (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

10 (C) INDIVIDUAL ISOLATE: G-Beta 4 (mouse), Fig. 26

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

15 Lys Lys Asx Glu Thr Asx Val Asn Met Gly Arg Tyr Thr Pro Arg Ile
 1 5 10 15

Lys His Ile Lys Arg Pro Arg Arg Thr Asp Xaa Xaa Gly
 20 25

20

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 718 amino acids

25 (B) TYPE: amino acid

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

30 (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

35 (C) INDIVIDUAL ISOLATE: GROUCHO PROTEIN DROSOPH, Fig. 27

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

40 Met Tyr Pro Ser Pro Val Arg His Pro Ala Ala Gly Gly Pro Pro Pro
 1 5 10 15

Gln Gly Pro Ile Lys Phe Thr Ile Ala Asp Thr Leu Glu Arg Ile Lys
 20 25 30

45

Glu Glu Phe Asn Phe Leu Gln Ala His Tyr His Ser Ile Lys Leu Glu

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	35		40		45
	Cys Glu Lys Leu Ser Asn Glu Lys Thr Glu Met Gln Arg His Tyr Val				
	50		55		60
5	Met Tyr Tyr Glu Met Ser Tyr Gly Leu Asn Val Glu Met His Lys Gln				
	65		70		75 80
	Thr Glu Ile Ala Lys Arg Leu Asn Thr Leu Ile Asn Gln Leu Leu Pro				
10		85		90	95
	Phe Leu Gln Ala Asp His Gln Gln Gln Val Leu Gln Ala Val Glu Arg				
		100		105	110
15	Ala Lys Gln Val Thr Met Gln Glu Leu Asn Leu Ile Ile Gly Gln Gln				
		115		120	125
	Ile His Ala Gln Gln Val Pro Gly Gly Pro Pro Gln Pro Met Gly Ala				
20		130		135	140
	Leu Asn Pro Phe Gly Ala Leu Gly Ala Thr Met Gly Leu Pro His Gly				
	145		150		155 160
	Pro Gln Gly Leu Leu Asn Lys Pro Pro Glu His His Arg Pro Asp Ile				
25		165		170	175
	Lys Pro Thr Gly Leu Glu Gly Pro Ala Ala Ala Glu Glu Arg Leu Arg				
		180		185	190
30	Asn Ser Val Ser Pro Ala Asp Arg Glu Lys Tyr Arg Thr Arg Ser Pro				
		195		200	205
	Leu Asp Ile Glu Asn Asp Ser Lys Arg Arg Lys Asp Glu Lys Leu Gln				
35		210		215	220
	Glu Asp Glu Gly Glu Lys Ser Asp Gln Asp Leu Val Val Asp Val Ala				
	225		230		235 240
	Asn Glu Met Glu Ser His Ser Pro Arg Pro Asn Gly Glu His Val Ser				
40		245		250	255
	Met Glu Val Arg Asp Arg Glu Ser Leu Asn Gly Glu Arg Leu Glu Lys				
		260		265	270
45	Pro Ser Ser Ser Gly Ile Lys Gln Glu Arg Pro Pro Ser Arg Ser Gly				
		275		280	285

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	Ser Ser Ser Ser Arg Ser Thr Pro Ser Leu Lys Thr Lys Asp Met Glu
	290 295 300
5	Lys Pro Gly Thr Pro Gly Ala Lys Ala Arg Thr Pro Thr Pro Asn Ala
	305 310 315 320
	Ala Ala Pro Ala Pro Gly Val Asn Pro Lys Gln Met Met Pro Gln Gly
	325 330 335
10	Pro Pro Pro Ala Gly Tyr Pro Gly Ala Pro Tyr Gln Arg Pro Ala Asp
	340 345 350
	Pro Tyr Gln Arg Pro Pro Ser Asp Pro Ala Tyr Gly Arg Pro Pro Pro
	355 360 365
15	Met Pro Tyr Asp Pro His Ala His Val Arg Thr Asn Gly Ile Pro His
	370 375 380
	Pro Ser Ala Leu Thr Gly Gly Lys Pro Ala Tyr Ser Phe His Met Asn
20	385 390 395 400
	Gly Glu Gly Ser Leu Gln Pro Val Pro Phe Pro Pro Asp Ala Leu Val
	405 410 415
25	Gly Val Gly Ile Pro Arg His Ala Arg Gln Ile Asn Thr Leu Ser His
	420 425 430
	Gly Glu Val Val Cys Ala Val Thr Ile Ser Asn Pro Thr Lys Tyr Val
	435 440 445
30	Tyr Thr Gly Gly Lys Gly Cys Val Lys Val Trp Asp Ile Ser Gln Pro
	450 455 460
	Gly Asn Lys Asn Pro Val Ser Gln Leu Asp Cys Leu Gln Arg Asp Asn
35	465 470 475 480
	Tyr Ile Arg Ser Val Lys Leu Leu Pro Asp Gly Arg Thr Leu Ile Val
	485 490 495
40	Gly Gly Glu Ala Ser Asn Leu Ser Ile Trp Asp Leu Ala Ser Pro Thr
	500 505 510
	Pro Arg Ile Lys Ala Glu Leu Thr Ser Ala Ala Pro Ala Cys Tyr Ala
45	515 520 525
	Leu Ala Ser Pro Asp Ser Lys Val Cys Phe Ser Cys Cys Ser Asp Gly

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	530	535	540
	Asn Ile Ala Val Trp Asp Leu His Asn Glu Ile Leu Val Arg Gln Phe		
	545	550	555 560
5	Gln Gly His Thr Asp Gly Ala Ser Cys Ile Asp Ile Ser Pro Asp Gly		
	565	570	575
	Ser Arg Leu Trp Thr Gly Gly Leu Asp Asn Thr Val Arg Ser Trp Asp		
10	580	585	590
	Leu Arg Glu Gly Arg Gln Leu Gln Gln His Asp Phe Ser Ser Gln Ile		
	595	600	605
15	Phe Ser Leu Gly Tyr Cys Pro Thr Gly Asp Trp Leu Ala Val Gly Met		
	610	615	620
	Glu Asn Ser His Val Glu Val Leu His Ala Ser Lys Pro Asp Lys Tyr		
	625	630	635 640
20	Gln Leu His Leu His Glu Ser Cys Val Leu Ser Leu Arg Phe Ala Ala		
	645	650	655
	Cys Gly Lys Trp Phe Val Ser Thr Gly Lys Asp Asn Leu Leu Asn Ala		
25	660	665	670
	Trp Arg Thr Pro Tyr Gly Ala Ser Ile Phe Gln Ser Lys Glu Thr Ser		
	675	680	685
30	Ser Val Leu Ser Cys Asp Ile Ser Thr Asp Asp Lys Tyr Ile Val Thr		
	690	695	700
	Gly Ser Gly Asp Lys Lys Ala Thr Val Tyr Glu Val Ile Tyr		
	705	710	715
35			

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 341 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

45

(iii) HYPOTHETICAL: NO

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(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: GTP binding protein (squid), Fig. 28

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

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Met Thr Ser Glu Leu Glu Ala Leu Arg Gln Glu Thr Glu Gln Leu Lys
 1 5 10 15

Asn Gln Ile Arg Glu Ala Arg Lys Ala Ala Ala Asp Thr Thr Leu Ala
 20 25 30

Met Ala Thr Ala Asn Val Glu Pro Val Gly Arg Ile Gln Met Arg Thr
 35 40 45

Arg Arg Thr Leu Arg Gly His Leu Ala Lys Ile Tyr Ala Met His Trp
 50 55 60

Ala Ser Asp Ser Arg Asn Leu Val Ser Ala Ser Gln Asp Gly Lys Leu
 65 70 75 80

Ile Val Trp Asp Gly Tyr Thr Thr Asn Lys Val His Ala Ile Pro Leu
 85 90 95

Arg Ser Ser Trp Val Met Thr Cys Ala Tyr Ala Pro Ser Gly Asn Tyr
 100 105 110

Val Ala Cys Gly Gly Leu Asp Asn Ile Cys Ser Ile Tyr Ser Leu Lys
 115 120 125

Thr Arg Glu Gly Asn Val Arg Val Ser Arg Glu Leu Pro Gly His Thr
 130 135 140

Gly Tyr Leu Ser Cys Cys Arg Phe Ile Asp Asp Asn Gln Ile Val Thr
 145 150 155 160

Ser Ser Gly Asp Met Thr Cys Ala Leu Trp Asn Ile Glu Thr Gly Asn
 165 170 175

Gln Ile Thr Ser Phe Gly Gly His Thr Gly Asp Val Met Ser Leu Ser
 180 185 190

Leu Ala Pro Asp Met Arg Thr Phe Val Ser Gly Ala Cys Asp Ala Ser
 195 200 205

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	Ala Lys Leu Phe Asp Ile Arg Asp Gly Ile Cys Lys Gln Thr Phe Thr
	210 215 220
5	Gly His Glu Ser Asp Ile Asn Ala Ile Thr Tyr Phe Pro Asn Gly Phe
	225 230 235 240
	Ala Phe Ala Thr Gly Ser Asp Asp Ala Thr Cys Arg Leu Phe Asp Ile
	245 250 255
10	Arg Ala Asp Gln Glu Ile Gly Met Tyr Ser His Asp Asn Ile Ile Cys
	260 265 270
	Gly Ile Thr Ser Val Ala Phe Ser Lys Ser Gly Arg Leu Leu Leu Gly
	275 280 285
15	Gly Tyr Asp Asp Phe Asn Cys Asn Val Trp Asp Val Leu Lys Gln Glu
	290 295 300
	Arg Ala Gly Val Leu Ala Gly His Asp Asn Arg Val Ser Cys Leu Gly
20	305 310 315 320
	Val Thr Glu Asp Gly Met Ala Val Ala Thr Gly Ser Trp Asp Ser Phe
	325 330 335
25	Leu Lys Ile Trp Asn
	340

(2) INFORMATION FOR SEQ ID NO:46:

- | | |
|----|---|
| 30 | (i) SEQUENCE CHARACTERISTICS: |
| | (A) LENGTH: 410 amino acids |
| | (B) TYPE: amino acid |
| | (D) TOPOLOGY: unknown |
| 35 | (ii) MOLECULE TYPE: protein |
| | (iii) HYPOTHETICAL: NO |
| | (iv) ANTI-SENSE: NO |
| 40 | (vi) ORIGINAL SOURCE: |
| | (C) INDIVIDUAL ISOLATE: IEF SSP 9306, Fig. 29 |
| 45 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO:46: |

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	Met	Ala	Asp	Lys	Glu	Ala	Ala	Phe	Asp	Asp	Ala	Val	Glu	Glu	Arg	Val	
	1				5					10					15		
5	Ile	Asn	Glu	Glu	Tyr	Lys	Ile	Trp	Lys	Lys	Asn	Thr	Pro	Phe	Leu	Tyr	
					20				25					30			
	Asp	Leu	Val	Met	Thr	His	Ala	Leu	Glu	Trp	Pro	Ser	Leu	Thr	Ala	Gln	
					35			40					45				
10	Trp	Leu	Pro	Asp	Val	Thr	Arg	Pro	Glu	Gly	Lys	Asp	Phe	Ser	Ile	His	
					50			55					60				
	Arg	Leu	Val	Leu	Gly	Thr	His	Thr	Ser	Asp	Glu	Gln	Asn	His	Leu	Val	
	65					70				75					80		
15	Ile	Ala	Ser	Val	Gln	Leu	Pro	Asn	Asp	Asp	Ala	Gln	Phe	Asp	Ala	Ser	
					85					90					95		
	His	Tyr	Asp	Ser	Glu	Lys	Gly	Glu	Phe	Gly	Gly	Phe	Gly	Ser	Val	Ser	
20					100				105					110			
	Gly	Lys	Ile	Glu	Ile	Glu	Ile	Lys	Ile	Asn	His	Glu	Gly	Glu	Val	Asn	
					115			120					125				
25	Arg	Ala	Arg	Tyr	Met	Pro	Gln	Asn	Pro	Cys	Ile	Ile	Ala	Thr	Lys	Thr	
					130			135					140				
	Pro	Ser	Ser	Asp	Val	Leu	Val	Phe	Asp	Tyr	Thr	Lys	His	Pro	Ser	Lys	
	145					150				155					160		
30	Pro	Asp	Pro	Ser	Gly	Glu	Cys	Asn	Pro	Asp	Leu	Arg	Leu	Arg	Gly	His	
					165					170					175		
	Gln	Lys	Glu	Gly	Tyr	Gly	Leu	Ser	Trp	Asn	Pro	Asn	Leu	Ser	Gly	His	
35					180				185					190			
	Leu	Leu	Ser	Ala	Ser	Asp	Asp	His	Thr	Ile	Cys	Leu	Trp	Asp	Ile	Ser	
					195			200					205				
40	Ala	Val	Pro	Lys	Glu	Gly	Lys	Val	Val	Asp	Ala	Lys	Thr	Ile	Phe	Thr	
					210			215					220				
	Gly	His	Thr	Ala	Val	Val	Glu	Asp	Val	Ser	Trp	His	Leu	Leu	His	Glu	
	225					230				235					240		
45	Ser	Leu	Phe	Gly	Ser	Val	Ala	Asp	Asp	Gln	Lys	Leu	Met	Ile	Trp	Asp	

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	245	250	255
	Thr Arg Ser Asn Asn Thr Ser Lys Pro Ser His Ser Val Asp Ala His		
	260	265	270
5	Thr Ala Glu Val Asn Cys Leu Ser Phe Asn Pro Tyr Ser Glu Phe Ile		
	275	280	285
	Leu Ala Thr Gly Ser Ala Asp Lys Thr Val Ala Leu Trp Asp Leu Arg		
10	290	295	300
	Asn Leu Lys Leu Lys Leu His Ser Phe Glu Ser His Lys Asp Glu Ile		
	305	310	315 320
15	Phe Gln Val Gln Trp Ser Pro His Asn Glu Thr Ile Leu Ala Ser Ser		
	325	330	335
	Gly Thr Asp Arg Arg Leu Asn Val Trp Asp Leu Ser Lys Ile Gly Glu		
	340	345	350
20	Glu Gln Ser Pro Glu Asp Ala Glu Asp Gly Pro Pro Glu Leu Leu Phe		
	355	360	365
	Ile His Gly Gly His Thr Ala Lys Ile Ser Asp Phe Ser Trp Asn Pro		
25	370	375	380
	Asn Glu Pro Trp Val Ile Cys Ser Val Ser Glu Asp Asn Ile Met Gln		
	385	390	395 400
30	Val Trp Gln Met Glu Leu Val Leu Asp His		
	405	410	

(2) INFORMATION FOR SEQ ID NO:47:

- 35 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 317 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: unknown
- 40 (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- 45 (vi) ORIGINAL SOURCE:

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(C) INDIVIDUAL ISOLATE: HUMAN 12.3, Fig. 30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

5	Met Thr Glu Gln Met Thr Leu Arg Gly Thr Leu Lys Gly His Asn Gly	
	1	15
10	Trp Val Thr Gln Ile Ala Thr Thr Pro Gln Phe Pro Asp Met Ile Leu	
	20	30
	Ser Ala Ser Arg Asp Lys Thr Ile Ile Met Trp Lys Leu Thr Arg Asp	
	35	45
15	Glu Thr Asn Tyr Gly Ile Pro Gln Arg Ala Leu Arg Gly His Ser His	
	50	60
	Phe Val Ser Asp Val Val Ile Ser Ser Asp Gly Gln Phe Ala Leu Ser	
	65	80
20	Gly Ser Trp Asp Gly Thr Leu Arg Leu Trp Asp Leu Thr Thr Gly Thr	
	85	95
	Thr Thr Arg Arg Phe Val Gly His Thr Lys Asp Val Leu Ser Val Ala	
25	100	110
	Phe Ser Ser Asp Asn Arg Gln Ile Val Ser Gly Ser Arg Asp Lys Thr	
	115	125
30	Ile Lys Leu Trp Asn Thr Leu Gly Val Cys Lys Tyr Thr Val Gln Asp	
	130	140
	Glu Ser His Ser Glu Trp Val Ser Cys Val Arg Phe Ser Pro Asn Ser	
	145	160
35	Ser Asn Pro Ile Ile Val Ser Cys Gly Trp Asp Lys Leu Val Lys Val	
	165	175
	Trp Asn Leu Ala Asn Cys Lys Leu Lys Thr Asn His Ile Gly His Thr	
40	180	190
	Gly Tyr Leu Asn Thr Val Thr Val Ser Pro Asp Gly Ser Leu Cys Ala	
	195	205
45	Ser Gly Gly Lys Asp Gly Gln Ala Met Leu Trp Asp Leu Asn Glu Gly	
	210	220

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Lys His Leu Tyr Thr Leu Asp Gly Gly Asp Ile Ile Asn Ala Leu Cys
 225 230 235 240
 Phe Ser Pro Asn Arg Tyr Trp Leu Cys Ala Ala Thr Gly Pro Ser Ile
 5 245 250 255
 Lys Ile Trp Asp Leu Glu Gly Lys Ile Ile Val Asp Glu Leu Lys Gln
 260 265 270
 10 Glu Val Ile Ser Thr Ser Ser Lys Ala Glu Pro Pro Gln Cys Thr Ser
 275 280 285
 Leu Ala Trp Ser Ala Asp Gly Gln Thr Leu Phe Ala Gly Tyr Thr Asp
 290 295 300
 15 Asn Leu Val Arg Val Trp Gln Val Thr Ile Gly Thr Arg
 305 310 315

(2) INFORMATION FOR SEQ ID NO:48:

20

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 425 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: unknown

25

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

30

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: IEF -7442 - human, Fig. 31

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

Met Ala Ser Lys Glu Met Phe Glu Asp Thr Val Glu Glu Arg Val Ile
 1 5 10 15
 40 Asn Glu Glu Tyr Lys Ile Trp Lys Lys Asn Thr Pro Phe Leu Tyr Asp
 20 25 30
 Leu Val Met Thr Thr His Ala Leu Gln Trp Pro Ser Leu Thr Val Gln Trp
 45 35 40 45

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	Leu Pro Glu Val Thr Lys Pro Glu Gly Lys Asp Tyr Ala Leu His Trp
	50 55 60
5	Leu Val Leu Gly Thr His Thr Ser Asp Glu Gln Asn His Leu Val Val
	65 70 75 80
	Ala Arg Val His Ile Pro Asn Asp Asp Ala Gln Phe Asp Ala Ser His
	85 90 95
10	Cys Asp Ser Asp Lys Gly Glu Phe Gly Gly Phe Gly Ser Val Thr Gly
	100 105 110
	Lys Ile Glu Cys Glu Ile Lys Ile Asn His Glu Gly Glu Val Asn Arg
	115 120 125
15	Ala Arg Tyr Met Pro Gln Asn Pro His Ile Ile Ala Thr Lys Thr Pro
	130 135 140
	Ser Ser Asp Val Leu Val Phe Asp Tyr Thr Lys His Pro Ala Lys Pro
20	145 150 155 160
	Asp Pro Ser Gly Glu Cys Asn Pro Asp Leu Arg Leu Arg Gly His Gln
	165 170 175
25	Lys Glu Gly Tyr Gly Leu Ser Trp Asn Ser Asn Leu Ser Gly His Leu
	180 185 190
	Leu Ser Ala Ser Asp Asp His Thr Val Cys Leu Trp Asp Ile Asn Ala
	195 200 205
30	Gly Pro Lys Glu Gly Lys Ile Val Asp Ala Lys Ala Ile Phe Thr Gly
	210 215 220
	His Ser Ala Val Val Glu Asp Val Ala Trp His Leu Leu His Glu Ser
35	225 230 235 240
	Leu Phe Gly Ser Val Ala Asp Asp Gln Lys Leu Met Ile Trp Asp Thr
	245 250 255
40	Arg Ser Asn Thr Thr Ser Lys Pro Ser His Leu Val Asp Ala His Thr
	260 265 270
	Ala Glu Val Asn Cys Leu Ser Phe Asn Pro Tyr Ser Glu Phe Ile Leu
	275 280 285
45	Ala Thr Gly Ser Ala Asp Lys Thr Val Ala Leu Trp Asp Leu Arg Asn

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	290		295		300
	Leu Lys Leu Lys Leu His Thr Phe Glu Ser His Lys Asp Glu Ile Phe				
	305		310		315 320
5	Gln Val His Trp Ser Pro His Asn Glu Thr Ile Leu Ala Ser Ser Gly				
		325		330	335
	Thr Asp Arg Arg Leu Asn Val Trp Asp Leu Ser Lys Ile Gly Glu Glu				
10		340		345	350
	Gln Ser Ala Glu Asp Ala Glu Asp Gly Pro Pro Glu Leu Leu Phe Ile				
		355		360	365
15	His Gly Gly His Thr Ala Lys Ile Ser Asp Phe Ser Trp Asn Pro Asn				
		370		375	380
	Glu Pro Trp Val Ile Cys Ser Val Ser Glu Asp Asn Ile Met Gln Ile				
		385		390	395 400
20	Trp Gln Met Ala Glu Asn Ile Tyr Asn Asp Glu Glu Ser Asp Val Thr				
		405		410	415
	Thr Ser Glu Leu Glu Gly Gln Gly Ser				
25		420		425	

(2) INFORMATION FOR SEQ ID NO:49:

	(i) SEQUENCE CHARACTERISTICS:
30	(A) LENGTH: 605 amino acids
	(B) TYPE: amino acid
	(D) TOPOLOGY: unknown
	(ii) MOLECULE TYPE: protein
35	
	(iii) HYPOTHETICAL: NO
	(iv) ANTI-SENSE: NO
40	(vi) ORIGINAL SOURCE:
	(C) INDIVIDUAL ISOLATE: Insulin-like growth factor binding protein complex, Fig. 32
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:
45	
	Met Ala Leu Arg Lys Gly Gly Leu Ala Leu Ala Leu Leu Leu Ser

1	5	10	15																
Trp	Val	Ala	Leu	Gly	Pro	Arg	Ser	Leu	Glu	Gly	Ala	Asp	Pro	Gly	Thr				
	20							25					30						
Pro	Gly	Glu	Ala	Glu	Gly	Pro	Ala	Cys	Pro	Ala	Ala	Cys	Val	Cys	Ser				
	35						40					45							
Tyr	Asp	Asp	Asp	Ala	Asp	Glu	Leu	Ser	Val	Phe	Cys	Ser	Ser	Arg	Asn				
	50					55					60								
Leu	Thr	Arg	Leu	Pro	Asp	Gly	Val	Pro	Gly	Gly	Thr	Gln	Ala	Leu	Trp				
65					70					75					80				
Leu	Asp	Gly	Asn	Asn	Leu	Ser	Ser	Val	Pro	Pro	Ala	Ala	Phe	Gln	Asn				
			85					90						95					
Leu	Ser	Ser	Leu	Gly	Phe	Leu	Asn	Leu	Gln	Gly	Gly	Gln	Leu	Gly	Ser				
	100						105					110							
Leu	Glu	Pro	Gln	Ala	Leu	Leu	Gly	Leu	Glu	Asn	Leu	Cys	His	Leu	His				
	115					120					125								
Leu	Glu	Arg	Asn	Gln	Leu	Arg	Ser	Leu	Ala	Leu	Gly	Thr	Phe	Ala	His				
	130				135					140									
Thr	Pro	Ala	Leu	Ala	Ser	Leu	Gly	Leu	Ser	Asn	Asn	Arg	Leu	Ser	Arg				
145					150					155					160				
Leu	Glu	Asp	Gly	Leu	Phe	Glu	Gly	Leu	Gly	Ser	Leu	Trp	Asp	Leu	Asn				
			165					170						175					
Leu	Gly	Trp	Asn	Ser	Leu	Ala	Val	Leu	Pro	Asp	Ala	Ala	Phe	Arg	Gly				
	180						185					190							
Leu	Gly	Ser	Leu	Arg	Glu	Leu	Val	Leu	Ala	Gly	Asn	Arg	Leu	Ala	Tyr				
	195					200					205								
Leu	Gln	Pro	Ala	Leu	Phe	Ser	Gly	Leu	Ala	Glu	Leu	Arg	Glu	Leu	Asp				
	210					215					220								
Leu	Ser	Arg	Asn	Ala	Leu	Arg	Ala	Ile	Lys	Ala	Asn	Val	Phe	Val	Gln				
225					230					235					240				
Leu	Pro	Arg	Leu	Gln	Lys	Leu	Tyr	Leu	Asp	Arg	Asn	Leu	Ile	Ala	Ala				
			245					250						255					

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	Val	Ala	Pro	Gly	Ala	Phe	Leu	Gly	Leu	Lys	Ala	Leu	Arg	Trp	Leu	Asp	
				260					265						270		
5	Leu	Ser	His	Asn	Arg	Val	Ala	Gly	Leu	Leu	Glu	Asp	Thr	Phe	Pro	Gly	
			275						280					285			
	Leu	Leu	Gly	Leu	Arg	Val	Leu	Arg	Leu	Ser	His	Asn	Ala	Ile	Ala	Ser	
			290					295					300				
10	Leu	Arg	Pro	Arg	Thr	Phe	Lys	Asp	Leu	His	Phe	Leu	Glu	Glu	Leu	Gln	
	305						310					315				320	
	Leu	Gly	His	Asn	Arg	Ile	Arg	Gln	Leu	Ala	Glu	Arg	Ser	Phe	Glu	Gly	
					325					330					335		
15	Leu	Gly	Gln	Leu	Glu	Val	Leu	Thr	Leu	Asp	His	Asn	Gln	Leu	Gln	Glu	
				340					345					350			
	Val	Lys	Ala	Gly	Ala	Phe	Leu	Gly	Leu	Thr	Asn	Val	Ala	Val	Met	Asn	
20			355					360					365				
	Leu	Ser	Gly	Asn	Cys	Leu	Arg	Asn	Leu	Pro	Glu	Gln	Val	Phe	Arg	Gly	
		370					375					380					
25	Leu	Gly	Lys	Leu	His	Ser	Leu	His	Leu	Glu	Gly	Ser	Cys	Leu	Gly	Arg	
	385					390					395					400	
	Ile	Arg	Pro	His	Thr	Phe	Thr	Gly	Leu	Ser	Gly	Leu	Arg	Arg	Leu	Phe	
					405					410					415		
30	Leu	Lys	Asp	Asn	Gly	Leu	Val	Gly	Ile	Glu	Glu	Gln	Ser	Leu	Trp	Gly	
				420					425					430			
	Leu	Ala	Glu	Leu	Leu	Glu	Leu	Asp	Leu	Thr	Ser	Asn	Gln	Leu	Thr	His	
35			435					440					445				
	Leu	Pro	His	Arg	Leu	Phe	Gln	Gly	Leu	Gly	Lys	Leu	Glu	Tyr	Leu	Leu	
			450				455					460					
40	Leu	Ser	Arg	Asn	Arg	Leu	Ala	Glu	Leu	Pro	Ala	Asp	Ala	Leu	Gly	Pro	
	465					470					475					480	
	Leu	Gln	Arg	Ala	Phe	Trp	Leu	Asp	Val	Ser	His	Asn	Arg	Leu	Glu	Ala	
					485					490					495		
45	Leu	Pro	Asn	Ser	Leu	Leu	Ala	Pro	Leu	Gly	Arg	Leu	Arg	Tyr	Leu	Ser	

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	500	505	510
	Leu Arg Asn Asn Ser Leu Arg Thr Phe Thr Pro Gln Pro Pro Gly Leu 515 520 525		
5	Glu Arg Leu Trp Leu Glu Gly Asn Pro Trp Asp Cys Gly Cys Pro Leu 530 535 540		
	Lys Ala Leu Arg Asp Phe Ala Leu Gln Asn Pro Ser Ala Val Pro Arg 545 550 555 560		
10	Phe Val Gln Ala Ile Cys Glu Gly Asp Asp Cys Gln Pro Pro Ala Tyr 565 570 575		
	Thr Tyr Asn Asn Ile Thr Cys Ala Ser Pro Pro Glu Val Val Gly Leu 580 585 590		
15	Asp Leu Arg Asp Leu Ser Glu Ala His Phe Ala Pro Cys 595 600 605		

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

25 (A) LENGTH: 603 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

30 (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

35 (C) INDIVIDUAL ISOLATE: Insulin-like growth factor bind.
pro. complex-rat, Fig. 33

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

40 Met Ala Leu Arg Thr Gly Gly Pro Ala Leu Val Val Leu Leu Ala Phe
1 5 10 15

Trp Val Ala Leu Gly Pro Cys His Leu Gln Gly Thr Asp Pro Gly Ala
20 25 30

45 Ser Ala Asp Ala Glu Gly Pro Gln Cys Pro Val Ala Cys Thr Cys Ser

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	35		40		45
	His Asp Asp Tyr Thr Asp Glu Leu Ser Val Phe Cys Ser Ser Lys Asn				
	50		55		60
5	Leu Thr His Leu Pro Asp Asp Ile Pro Val Ser Thr Arg Ala Leu Trp				
	65		70		75 80
	Leu Asp Gly Asn Asn Leu Ser Ser Ile Pro Ser Ala Ala Phe Gln Asn				
10		85		90	95
	Leu Ser Ser Leu Asp Phe Leu Asn Leu Gln Gly Ser Trp Leu Arg Ser				
		100		105	110
15	Leu Glu Pro Gln Ala Leu Leu Gly Leu Gln Asn Leu Tyr Tyr Leu His				
		115		120	125
	Leu Glu Arg Asn Arg Leu Arg Asn Leu Ala Val Gly Leu Phe Thr His				
		130		135	140
20	Thr Pro Ser Leu Ala Ser Leu Ser Leu Ser Ser Asn Leu Leu Gly Arg				
		145		150	155 160
	Leu Glu Glu Gly Leu Phe Gln Gly Leu Ser His Leu Trp Asp Leu Asn				
25		165		170	175
	Leu Gly Trp Asn Ser Leu Val Val Leu Pro Asp Thr Val Phe Gln Gly				
		180		185	190
30	Leu Gly Asn Leu His Glu Leu Val Leu Ala Gly Asn Lys Leu Thr Tyr				
		195		200	205
	Leu Gln Pro Ala Leu Phe Cys Gly Leu Gly Glu Leu Arg Glu Leu Asp				
		210		215	220
35	Leu Ser Arg Asn Ala Leu Arg Ser Val Lys Ala Asn Val Phe Val His				
		225		230	235 240
	Leu Pro Arg Leu Gln Lys Leu Tyr Leu Asp Arg Asn Leu Ile Thr Ala				
40		245		250	255
	Val Ala Pro Gly Ala Phe Leu Gly Met Lys Ala Leu Arg Trp Leu Asp				
		260		265	270
45	Leu Ser His Asn Arg Val Ala Gly Leu Met Glu Asp Thr Phe Pro Gly				
		275		280	285

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	Leu Leu Gly Leu His Val Leu Arg Leu Ala His Asn Ala Ile Ala Ser
	290 295 300
5	Leu Arg Pro Arg Thr Phe Lys Asp Leu His Phe Leu Glu Glu Leu Gln
	305 310 315 320
	Leu Gly His Asn Arg Ile Arg Gln Leu Gly Glu Arg Thr Phe Glu Gly
	325 330 335
10	Leu Gly Gln Leu Glu Val Leu Thr Leu Asn Asp Asn Gln Ile Thr Glu
	340 345 350
	Val Arg Val Gly Ala Phe Ser Gly Leu Phe Asn Val Ala Val Met Asn
15	355 360 365
	Leu Ser Gly Asn Cys Leu Arg Ser Leu Pro Glu Arg Val Phe Gln Gly
	370 375 380
20	Leu Asp Lys Leu His Ser Leu His Leu Glu His Ser Cys Leu Gly His
	385 390 395 400
	Val Arg Leu His Thr Phe Ala Gly Leu Ser Gly Leu Arg Arg Leu Phe
	405 410 415
25	Leu Arg Asp Asn Ser Ile Ser Ser Ile Glu Glu Gln Ser Leu Ala Gly
	420 425 430
	Leu Ser Glu Leu Leu Glu Leu Asp Leu Thr Thr Asn Arg Leu Thr His
30	435 440 445
	Leu Pro Arg Gln Leu Phe Gln Gly Leu Gly His Leu Glu Tyr Leu Leu
	450 455 460
35	Leu Ser Tyr Asn Gln Leu Thr Thr Leu Ser Ala Glu Val Leu Gly Pro
	465 470 475 480
	Leu Gln Arg Ala Phe Trp Leu Asp Ile Ser His Asn His Leu Glu Thr
	485 490 495
40	Leu Ala Glu Gly Leu Phe Ser Ser Leu Gly Arg Val Arg Tyr Leu Ser
	500 505 510
	Leu Arg Asn Asn Ser Leu Gln Thr Phe Ser Pro Gln Pro Gly Leu Glu
45	515 520 525
	Arg Leu Trp Leu Asp Ala Asn Pro Trp Asp Cys Ser Cys Pro Leu Lys

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	530		535		540	
	Ala Leu Arg Asp Phe	Ala Leu Gln Asn Pro Gly Val Val	Pro Arg Phe			
	545	550	555	560		
5	Val Gln Thr Val Cys Glu Gly Asp Asp Cys Gln Pro Val Tyr Thr Tyr					
		565	570	575		
	Asn Asn Ile Thr Cys Ala Gly Pro Ala Asn Val Ser Gly Leu Asp Leu					
10		580	585	590		
	Arg Asp Val Ser Glu Thr His Phe Val His Cys					
	595	600				

15 (2) INFORMATION FOR SEQ ID NO:51:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 409 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
- (C) INDIVIDUAL ISOLATE: LIS1 (human), Fig. 34

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

35	Met Val Leu Ser Gln Arg Gln Arg Asp Glu Leu Asn Arg Ala Ile Ala		
	1	5	10 15
	Asp Tyr Leu Arg Ser Asn Gly Tyr Glu Glu Ala Tyr Ser Val Phe Lys		
	20	25	30
40	Lys Glu Ala Glu Leu Asp Val Asn Glu Glu Leu Asp Lys Lys Tyr Ala		
	35	40	45
	Gly Leu Leu Glu Lys Lys Trp Thr Ser Val Ile Arg Leu Gln Lys Lys		
	50	55	60
45	Val Met Glu Leu Glu Ser Lys Leu Asn Glu Ala Lys Glu Glu Phe Thr		

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	65		70		75		80
	Ser Gly Gly Pro Leu Gly Gln Lys Arg Asp Pro Lys Glu Trp Ile Pro						
		85		90		95	
5	Arg Pro Pro Glu Lys Tyr Ala Leu Ser Gly His Arg Ser Pro Val Thr						
		100		105		110	
	Arg Val Ile Phe His Pro Val Phe Ser Val Met Val Ser Ala Ser Glu						
10		115		120		125	
	Asp Ala Thr Ile Lys Val Trp Asp Tyr Glu Thr Gly Asp Phe Glu Arg						
		130		135		140	
15	Thr Leu Lys Gly His Thr Asp Ser Val Gln Asp Ile Ser Phe Asp His						
		145		150		155	160
	Ser Gly Lys Leu Leu Ala Ser Cys Ser Ala Asp Met Thr Ile Lys Leu						
		165		170		175	
20	Trp Asp Phe Gln Gly Phe Glu Cys Ile Arg Thr Met His Gly His Asp						
		180		185		190	
	His Asn Val Ser Ser Val Ala Ile Met Pro Asn Gly Asp His Ile Val						
25		195		200		205	
	Ser Ala Ser Arg Asp Lys Thr Ile Lys Met Trp Glu Val Gln Thr Gly						
		210		215		220	
30	Tyr Cys Val Lys Thr Phe Thr Gly His Arg Glu Trp Val Arg Met Val						
		225		230		235	240
	Arg Pro Asn Gln Asp Gly Thr Leu Ile Ala Ser Cys Ser Asn Asp Gln						
		245		250		255	
35	Thr Val Arg Val Trp Val Val Ala Thr Lys Glu Cys Lys Ala Glu Leu						
		260		265		270	
	Arg Glu His Glu His Val Val Glu Cys Ile Ser Trp Ala Pro Glu Ser						
40		275		280		285	
	Ser Tyr Ser Ser Ile Ser Glu Ala Thr Gly Ser Glu Thr Lys Lys Ser						
		290		295		300	
45	Gly Lys Pro Gly Pro Phe Leu Leu Ser Gly Ser Arg Asp Lys Thr Lys						
		305		310		315	320

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Met Trp Asp Val Ser Thr Gly Met Cys Leu Met Thr Leu Val Gly His
325 330 335

Asp Asn Trp Val Arg Gly Val Leu Phe His Ser Gly Gly Lys Phe Ile
5 340 345 350

Leu Ser Cys Ala Asp Asp Lys Thr Leu Arg Val Trp Asp Tyr Lys Asn
355 360 365

10	Lys Arg Cys Met Lys Thr Leu Asn Ala His Glu His Phe Val Thr Ser
	370 375 380

Leu Asp Phe His Lys Thr Ala Pro Tyr Val Val Thr Gly Ser Val Asp
385 390 395 400

15 Gln Thr Val Lys Val Trp Glu Cys Arg
405

(2) INFORMATION FOR SEQ ID NO:52:

20

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 422 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: unknown

25

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

30 (iv) ANTI-SENSE: NO .

(vi) ORIGINAL SOURCE:
(c) INDIVIDUAL ISOLATE: MD6, Fig. 35

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

Met Glu Arg Lys Asp Phe Glu Thr Trp Leu Asp Asn Ile Ser Val Thr
1 5 10 15

Phe Leu Ser Leu Met Asp Leu Gln Lys Asn Glu Thr Leu Asp His Leu
20 25 30

Ile Ser Leu Ser Gly Ala Val Gln Leu Arg His Leu Ser Asn Asn Leu
45 35 40 45

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	Glu Thr Leu Leu Lys Arg Asp Phe Leu Lys Leu Leu Pro Leu Glu Leu	
	50	55 60
5	Ser Phe Tyr Leu Leu Lys Trp Leu Asp Pro Gln Thr Leu Leu Thr Cys	
	65	70 75 80
	Cys Leu Val Ser Lys Gln Arg Asn Lys Val Ile Ser Ala Cys Thr Glu	
		85 90 95
10	Val Trp Gln Thr Ala Cys Lys Asn Leu Gly Trp Gln Ile Asp Asp Ser	
		100 105 110
	Val Gln Asp Ser Leu His Trp Lys Lys Val Tyr Leu Lys Ala Ile Leu	
		115 120 125
15	Arg Met Lys Gln Leu Glu Asp His Glu Ala Phe Glu Thr Ser Ser Leu	
		130 135 140
	Ile Gly His Ser Ala Arg Val Tyr Ala Leu Tyr Tyr Lys Asp Gly Leu	
20		145 150 155 160
	Leu Cys Thr Gly Ser Asp Asp Leu Ser Ala Lys Leu Trp Asp Val Ser	
		165 170 175
25	Thr Gly Gln Cys Val Tyr Gly Ile Gln Thr His Thr Cys Ala Ala Val	
		180 185 190
	Lys Phe Asp Glu Gln Lys Leu Val Thr Gly Ser Phe Asp Asn Thr Val	
		195 200 205
30	Ala Cys Trp Glu Trp Ser Ser Gly Ala Arg Thr Gln His Phe Arg Gly	
		210 215 220
	His Thr Gly Ala Val Phe Ser Val Asp Tyr Ser Asp Glu Leu Asp Ile	
35		225 230 235 240
	Leu Val Ser Gly Ser Ala Asp Phe Ala Val Lys Val Trp Ala Leu Ser	
		245 250 255
40	Ala Gly Thr Cys Leu Asn Thr Leu Thr Gly His Thr Glu Trp Val Thr	
		260 265 270
	Lys Val Val Leu Gln Lys Cys Lys Val Lys Ser Leu Leu His Ser Pro	
		275 280 285
45	Gly Asp Tyr Ile Leu Leu Ser Ala Asp Lys Tyr Glu Ile Lys Ile Trp	

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	290		295		300
	Pro Ile Gly Arg Glu Ile Asn Cys Lys Cys Leu Lys Thr Leu Ser Val				
	305		310		315 320
5	Ser Glu Asp Arg Ser Ile Cys Leu Gln Pro Arg Leu His Phe Asp Gly				
		325		330	335
	Lys Tyr Ile Val Cys Ser Ser Ala Leu Gly Leu Tyr Gln Trp Asp Phe				
10		340		345	350
	Ala Ser Tyr Asp Ile Leu Arg Val Ile Lys Thr Pro Glu Val Ala Asn				
		355		360	365
15	Leu Ala Leu Leu Gly Phe Gly Asp Val Phe Ala Leu Leu Phe Asp Asn				
		370		375	380
	His Tyr Leu Tyr Ile Met Asp Leu Arg Thr Glu Ser Leu Ile Ser Arg				
		385		390	395 400
20	Trp Pro Leu Pro Glu Tyr Arg Lys Ser Lys Arg Gly Thr Ser Phe Leu				
		405		410	415
	Ala Gly Glu Arg Pro Gly				
25		420			

(2) INFORMATION FOR SEQ ID NO:53:

	(i) SEQUENCE CHARACTERISTICS:
30	(A) LENGTH: 422 amino acids
	(B) TYPE: amino acid
	(D) TOPOLOGY: unknown
	(ii) MOLECULE TYPE: protein
35	
	(iii) HYPOTHETICAL: NO
	(iv) ANTI-SENSE: NO
40	(vi) ORIGINAL SOURCE:
	(C) INDIVIDUAL ISOLATE: MSL1, Fig. 36
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:
45	
	Met Asn Gln Cys Ala Lys Asp Ile Thr His Glu Ala Ser Ser Ile Pro

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	1		5		10		15									
	Ile	Asp	Leu	Gln	Glu	Arg	Tyr	Ser	His	Trp	Lys	Lys	Asn	Thr	Lys	Leu
			20					25					30			
5																
	Leu	Tyr	Asp	Tyr	Leu	Asn	Thr	Asn	Ser	Thr	Lys	Trp	Pro	Ser	Leu	Thr
			35					40					45			
10	Cys	Gln	Phe	Phe	Pro	Asp	Leu	Asp	Thr	Thr	Ser	Asp	Glu	His	Arg	Ile
			50				55					60				
	Leu	Leu	Ser	Ser	Phe	Thr	Ser	Ser	Gln	Lys	Pro	Glu	Asp	Glu	Thr	Ile
	65					70				75					80	
15	Tyr	Ile	Ser	Lys	Ile	Ser	Thr	Leu	Gly	His	Ile	Lys	Trp	Ser	Ser	Leu
										85			90		95	
	Asn	Asn	Phe	Asp	Met	Asp	Glu	Met	Glu	Phe	Lys	Pro	Glu	Asn	Ser	Thr
							100			105				110		
20																
	Arg	Phe	Pro	Ser	Lys	His	Leu	Val	Asn	Asp	Ile	Ser	Ile	Phe	Phe	Pro
							115			120			125			
	Asn	Gly	Glu	Cys	Asn	Arg	Ala	Arg	Tyr	Leu	Pro	Gln	Asn	Pro	Asp	Ile
25			130				135					140				
	Ile	Ala	Gly	Ala	Ser	Ser	Asp	Gly	Ala	Ile	Tyr	Ile	Phe	Asp	Arg	Thr
	145					150				155					160	
30	Lys	His	Gly	Ser	Thr	Arg	Ile	Arg	Gln	Ser	Lys	Ile	Ser	His	Pro	Phe
						165				170				175		
	Glu	Thr	Lys	Leu	Phe	Gly	Ser	His	Gly	Val	Ile	Gln	Asp	Val	Glu	Ala
						180			185				190			
35																
	Met	Asp	Thr	Ser	Ser	Ala	Asp	Ile	Asn	Glu	Ala	Thr	Ser	Leu	Ala	Trp
						195			200				205			
	Asn	Leu	Gln	Gln	Glu	Ala	Leu	Leu	Leu	Ser	Ser	His	Ser	Asn	Gly	Gln
40			210				215					220				
	Val	Gln	Val	Trp	Asp	Ile	Lys	Gln	Tyr	Ser	His	Glu	Asn	Pro	Ile	Ile
	225					230				235					240	
45	Asp	Leu	Pro	Leu	Val	Ser	Ile	Asn	Ser	Asp	Gly	Thr	Ala	Val	Asn	Asp
						245				250				255		

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	Val Thr Trp Met Pro Thr His Asp Ser Leu Phe Ala Ala Cys Thr Glu	
	260	265 270
5	Gly Asn Ala Val Ser Leu Leu Asp Leu Arg Thr Lys Lys Glu Lys Leu	
	275	280 285
	Gln Ser Asn Arg Glu Lys His Asp Gly Gly Val Asn Ser Cys Arg Phe	
	290	295 300
10	Asn Tyr Lys Asn Ser Leu Ile Leu Ala Ser Ala Asp Ser Asn Gly Arg	
	305	310 315 320
	Leu Asn Leu Trp Asp Ile Arg Asn Met Asn Lys Ser Pro Ile Ala Thr	
15	325	330 335
	Met Glu His Gly Thr Ser Val Ser Thr Leu Glu Trp Ser Pro Asn Phe	
	340	345 350
	Asp Thr Val Leu Ala Thr Ala Gly Gln Glu Asp Gly Leu Val Lys Leu	
20	355	360 365
	Trp Asp Thr Ser Cys Glu Glu Thr Ile Phe Thr His Gly Gly His Met	
	370	375 380
25	Leu Gly Val Asn Asp Ile Ser Trp Asp Ala His Asp Pro Trp Leu Met	
	385	390 395 400
	Cys Ser Val Ala Asn Asp Asn Ser Val His Ile Trp Lys Pro Ala Gly	
	405	410 415
30	Asn Leu Val Gly His Ser	
	420	

(2) INFORMATION FOR SEQ ID NO:54:

35

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 816 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: unknown

40

- (ii) MOLECULE TYPE: protein

- (iii) HYPOTHETICAL: NO

45

- (iv) ANTI-SENSE: NO

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(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: MUS MUSCULUS PROTEIN, Fig. 37

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

```

Phe Arg Met Asp Asn Ala Ser Thr Arg Ile Asp Glu Arg Phe Arg Ile
1           5           10           15

10 Asp Ala Tyr Ala Asn Ala Arg Tyr Pro Met Pro Arg Thr Glu Ile Asn
    20           25           30

Ser Glu Gln Glu Asn Cys Glu Asn Thr Ile Thr Leu Glu Asp Ser Glu
    35           40           45

15 Gln Glu Asn Cys Glu Ala Ala Cys Met Pro Leu Glu Thr Glu Ser Glu
    50           55           60

Gln Glu Asn Cys Glu Met Ser Ser His Glu Ser Tyr Thr Asn Ala Ala
20 65           70           75           80

Glu Thr Pro Glu Asn Ile Ser Ile Leu Ser Cys Leu Gly Glu Thr Ser
    85           90           95

25 Gly Ala Leu Val Asp Thr Lys Thr Ile Ser Asp Ile Lys Thr Met Asp
    100          105          110

Pro Arg Val Ser Leu Thr Pro Ser Ser Asp Val Thr Gly Thr Glu Asp
    115          120          125

30 Ser Ser Val Leu Thr Pro Gln Ser Thr Asp Val Asn Ser Val Asp Ser
    130          135          140

Tyr Gln Gly Tyr Glu Gly Asp Asp Asp Asp Glu Glu Asp Asp Glu Asp
35 145          150          155          160

Asp Lys Asp Gly Asp Ser Asn Leu Pro Ser Leu Glu Asp Ser Asp Asn
    165          170          175

40 Phe Ile Ser Cys Leu Glu Asn Ser Tyr Ile Pro Gln Asn Val Glu Asn
    180          185          190

Gly Glu Val Val Glu Glu Gln Ser Leu Gly Arg Arg Phe His Pro Tyr
    195          200          205

45 Glu Leu Glu Ala Gly Glu Val Val Glu Gly Gln Gly Gly Ser Leu

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	210	215	220
	Phe Tyr Pro Tyr Glu Leu Glu Ala Gly Glu Val Val Glu Ala Gln Asn		
	225	230	235 240
5	Val Gln Asn Leu Phe His Arg Tyr Glu Leu Glu Glu Gly Glu Val Val		
	245	250	255
	Glu Ala Gln Val Val Gln Ser Met Phe Pro Tyr Tyr Glu Leu Glu Ala		
10	260	265	270
	Gly Glu Val Val Glu Ala Glu Glu Val Gln Gly Phe Phe Gln Arg Tyr		
	275	280	285
15	Glu Leu Glu Ala Arg Glu Val Ile Gly Ala Gln Gly Gly Gln Gly Leu		
	290	295	300
	Ser Arg His Tyr Gly Leu Glu Gly Gly Glu Val Val Glu Ala Thr Ala		
	305	310	315 320
20	Val Arg Arg Leu Ile Gln His His Glu Leu Glu Glu Gly Glu Asp Val		
	325	330	335
	Asp Asp Gln Glu Glu Ser Ser Glu Met His Glu Glu Thr Ser Glu Asp		
25	340	345	350
	Ser Ser Glu Gln Tyr Asp Ile Glu Asp Asp Ser Leu Ile Asp Glu Trp		
	355	360	365
30	Ile Ala Leu Glu Thr Ser Pro Leu Pro Arg Pro Arg Trp Asn Val Leu		
	370	375	380
	Ser Ala Leu Arg Asp Arg Gln Leu Gly Ser Ser Gly Arg Phe Val Tyr		
	385	390	395 400
35	Glu Ala Cys Gly Ala Arg Leu Phe Val Gln Arg Phe Ser Leu Glu His		
	405	410	415
	Val Phe Glu Gly His Ser Gly Cys Val Asn Thr Val His Phe Asn Gln		
40	420	425	430
	His Gly Thr Leu Leu Ala Ser Gly Ser Asp Asp Leu Lys Val Ile Val		
	435	440	445
45	Trp Asp Trp Leu Lys Lys Arg Ser Val Leu Asn Phe Asp Ser Gly His		
	450	455	460

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	Lys Asn Asn Ile Leu Gln Ala Lys Phe Leu Pro Asn Cys Asn Asp Ala	
	465	470 475 480
5	Ile Leu Ala Met Cys Gly Arg Asp Gly Gln Val Arg Val Ala Gln Leu	
	485	490 495
	Ser Ala Val Ala Gly Thr His Met Thr Lys Arg Leu Val Lys His Gly	
	500	505 510
10	Gly Ala Ser His Arg Leu Gly Leu Glu Pro Asp Ser Pro Phe Arg Phe	
	515	520 525
	Leu Thr Ser Gly Glu Asp Ala Val Val Phe Asn Ile Asp Leu Arg Gln	
15	530	535 540
	Ala His Pro Ala Ser Lys Leu Leu Val Ile Lys Asp Gly Asp Lys Lys	
	545	550 555 560
	Val Gly Leu Tyr Thr Val Phe Val Asn Pro Ala Asn Val Tyr Gln Phe	
20	565	570 575
	Ala Val Gly Gly Gln Asp Gln Phe Met Arg Ile Tyr Asp Gln Arg Lys	
	580	585 590
25	Ile Asp Glu Asn Val Asn Asn Gly Val Leu Lys Lys Phe Cys Pro His	
	595	600 605
	His Leu Leu Ser Ser Asp Tyr Pro Ala His Ile Thr Ser Leu Met Tyr	
30	610	615 620
	Ser Tyr Asp Gly Thr Glu Ile Leu Ala Ser Tyr Asn Asp Glu Asp Ile	
	625	630 635 640
	Tyr Ile Phe Asn Ser Ser Asp Ser Asp Gly Ala Gln Tyr Ala Lys Arg	
35	645	650 655
	Tyr Lys Gly His Arg Asn Asn Ser Thr Val Lys Gly Val Tyr Phe Tyr	
	660	665 670
40	Gly Pro Arg Ser Glu Phe Val Met Ser Gly Ser Asp Cys Gly His Ile	
	675	680 685
	Phe Ile Trp Glu Lys Ser Ser Cys Gln Ile Val Gln Phe Leu Glu Ala	
45	690	695 700
	Asp Glu Gly Gly Thr Ile Asn Cys Ile Asp Ser His Pro Tyr Leu Pro	

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[illegible]

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 422 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

30

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

35 (vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: ORF RB1, Fig. 38

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

40

Met Asn Gln Cys Ala Lys Asp Ile Thr His Glu Ala Ser Ser Ile Pro
1 5 10 15

Ile Asp Leu Gln Glu Arg Tyr Ser His Trp Lys Lys Asn Thr Lys Leu
45 20 25 30

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	Leu Tyr Asp Tyr Leu Asn Thr Asn Ser Thr Lys Trp Pro Ser Leu Thr
	35 40 45
5	Cys Gln Phe Phe Pro Asp Leu Asp Thr Thr Ser Asp Glu His Arg Ile
	50 55 60
	Leu Leu Ser Ser Phe Thr Ser Ser Gln Lys Pro Glu Asp Glu Thr Ile
	65 70 75 80
10	Tyr Ile Ser Lys Ile Ser Thr Leu Gly His Ile Lys Trp Ser Ser Leu
	85 90 95
	Asn Asn Phe Asp Met Asp Glu Met Glu Phe Lys Pro Glu Asn Ser Thr
	100 105 110
15	Arg Phe Pro Ser Lys His Leu Val Asn Asp Ile Ser Ile Phe Phe Pro
	115 120 125
	Asn Gly Glu Cys Asn Arg Ala Arg Tyr Leu Pro Gln Asn Pro Asp Ile
20	130 135 140
	Ile Ala Gly Ala Ser Ser Asp Gly Ala Ile Tyr Ile Phe Asp Arg Thr
	145 150 155 160
25	Lys His Gly Ser Thr Arg Ile Arg Gln Ser Lys Ile Ser His Pro Phe
	165 170 175
	Glu Thr Lys Leu Phe Gly Ser His Gly Val Ile Gln Asp Val Glu Ala
	180 185 190
30	Met Asp Thr Ser Ser Ala Asp Ile Asn Glu Ala Thr Ser Leu Ala Trp
	195 200 205
	Asn Leu Gln Gln Glu Ala Leu Leu Leu Ser Ser His Ser Asn Gly Gln
35	210 215 220
	Val Gln Val Trp Asp Ile Lys Gln Tyr Ser His Glu Asn Pro Ile Ile
	225 230 235 240
40	Asp Leu Pro Leu Val Ser Ile Asn Ser Asp Gly Thr Ala Val Asn Asp
	245 250 255
	Val Thr Trp Met Pro Thr His Asp Ser Leu Phe Ala Ala Cys Thr Glu
	260 265 270
45	Gly Asn Ala Val Ser Leu Leu Asp Leu Arg Thr Lys Lys Glu Lys Leu

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	275		280		285
	Gln Ser Asn Arg Glu Lys His Asp Gly Gly Val Asn Ser Cys Arg Phe				
	290		295		300
5	Asn Tyr Lys Asn Ser Leu Ile Leu Ala Ser Ala Asp Ser Asn Gly Arg				
	305		310		320
	Leu Asn Leu Trp Asp Ile Arg Asn Met Asn Lys Ser Pro Ile Ala Thr				
10		325		330	335
	Met Glu His Gly Thr Ser Val Ser Thr Leu Glu Trp Ser Pro Asn Phe				
		340		345	350
15	Asp Thr Val Leu Ala Thr Ala Gly Gln Glu Asp Gly Leu Val Lys Leu				
		355		360	365
	Trp Asp Thr Ser Cys Glu Glu Thr Ile Phe Thr His Gly Gly His Met				
		370		375	380
20	Leu Gly Val Asn Asp Ile Ser Trp Asp Ala His Asp Pro Trp Leu Met				
		385		390	395
	Cys Ser Val Ala Asn Asp Asn Ser Val His Ile Trp Lys Pro Ala Gly				
25		405		410	415
	Asn Leu Val Gly His Ser				
		420			

30 (2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 576 amino acids

(B) TYPE: amino acid

35 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

40

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Periodic Trp protein, Fig. 39

45

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

	Met	Ile	Ser	Ala	Thr	Asn	Trp	Val	Pro	Arg	Gly	Phe	Ser	Ser	Glu	Phe	
	1				5					10					15		
5																	
	Pro	Glu	Lys	Tyr	Val	Leu	Asp	Asp	Glu	Glu	Val	Glu	Arg	Ile	Asn	Gln	
					20				25						30		
	Leu	Ala	Gln	Leu	Asn	Leu	Asp	Asp	Ala	Lys	Ala	Thr	Leu	Glu	Glu	Ala	
10					35				40					45			
	Glu	Gly	Glu	Ser	Gly	Val	Glu	Asp	Asp	Ala	Ala	Thr	Gly	Ser	Ser	Asn	
					50				55					60			
15	Lys	Leu	Lys	Asp	Gln	Leu	Asp	Ile	Asp	Asp	Asp	Leu	Lys	Glu	Tyr	Asn	
	65					70					75					80	
	Leu	Glu	Glu	Tyr	Asp	Asp	Glu	Glu	Ile	Ala	Asp	Asn	Glu	Gly	Gly	Lys	
					85					90					95		
20																	
	Asp	Val	Ser	Met	Phe	Pro	Gly	Leu	Ser	Asn	Asp	Ser	Asp	Val	Lys	Phe	
					100					105					110		
	His	Glu	Gly	Glu	Lys	Gly	Glu	Asp	Pro	Tyr	Ile	Ser	Leu	Pro	Asn	Gln	
25					115					120				125			
	Glu	Asp	Ser	Gln	Glu	Glu	Lys	Gln	Glu	Leu	Gln	Val	Tyr	Pro	Ser	Asp	
					130				135					140			
30	Asn	Leu	Val	Leu	Ala	Ala	Arg	Thr	Glu	Asp	Asp	Val	Ser	Tyr	Leu	Asp	
	145					150					155					160	
	Ile	Tyr	Val	Tyr	Asp	Asp	Gly	Ala	Gly	Phe	His	Ser	Ser	Asp	Ile	Pro	
					165					170					175		
35																	
	Val	Glu	Glu	Gly	Asp	Glu	Ala	Asp	Pro	Asp	Val	Ala	Arg	Gly	Leu	Val	
					180					185					190		
	Arg	Asp	Pro	Ala	Leu	Tyr	Val	His	His	Asp	Leu	Met	Leu	Pro	Ala	Phe	
40					195					200				205			
	Pro	Leu	Cys	Val	Glu	Trp	Leu	Asp	Tyr	Lys	Val	Gly	Ser	Asn	Ser	Glu	
					210				215					220			
45	Glu	Ala	Ala	Asn	Tyr	Ala	Ala	Ile	Gly	Thr	Phe	Asp	Pro	Gln	Ile	Glu	
	225					230					235					240	

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	Ile Trp Asn Leu Asp Cys Val Asp Lys Ala Phe Pro Asp Met Ile Leu	
	245	250 255
5	Gly Glu Pro Leu Asp Asn Ser Met Val Ser Leu Lys Ser Lys Lys Lys	
	260	265 270
	Lys Lys Lys Ser Lys Thr Gly His Ile Thr Thr His His Thr Asp Ala	
	275	280 285
10	Val Leu Ser Met Ala His Asn Lys Tyr Phe Arg Ser Val Leu Ala Ser	
	290	295 300
	Thr Ser Ala Asp His Thr Val Lys Leu Trp Asp Leu Asn Ser Gly Asn	
15	305	310 315 320
	Ala Ala Arg Ser Leu Ala Ser Ile His Ser Asn Lys Asn Val Ser Ser	
	325	330 335
	Ser Glu Trp His Met Leu Asn Gly Ser Ile Leu Leu Thr Gly Gly Tyr	
20	340	345 350
	Asp Ser Arg Val Ala Leu Thr Asp Val Arg Ile Ser Asp Glu Ser Gln	
	355	360 365
25	Met Ser Lys Tyr Trp Ser Ala Met Ala Gly Glu Glu Ile Glu Thr Val	
	370	375 380
	Thr Phe Ala Ser Glu Asn Ile Ile Leu Cys Gly Thr Asp Ser Gly Asn	
30	385	390 395 400
	Val Tyr Ser Phe Asp Ile Arg Asn Asn Glu Asn Arg Lys Pro Val Trp	
	405	410 415
	Thr Leu Lys Ala His Asp Ala Gly Ile Ser Thr Leu Cys Ser Asn Lys	
35	420	425 430
	Phe Ile Pro Gly Met Met Ser Thr Gly Ala Met Gly Glu Lys Thr Val	
	435	440 445
40	Lys Leu Trp Lys Phe Pro Leu Asp Asp Ala Thr Asn Thr Lys Gly Pro	
	450	455 460
	Ser Met Val Leu Ser Arg Asp Phe Asp Val Gly Asn Val Leu Thr Ser	
45	465	470 475 480
	Ser Phe Ala Pro Asp Ile Glu Val Ala Gly Thr Met Val Ile Gly Gly	

495

Asn Asp His Asn Ile Cys Ile Phe Ser Leu Asp Ser Pro Met Pro Leu
35 40 45

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	Tyr	Ile	Leu	Lys	Gly	His	Lys	Asp	Thr	Val	Cys	Ser	Leu	Ser	Ser	Gly	
	50						55					60					
5	Lys	Phe	Gly	Thr	Leu	Leu	Ser	Gly	Ser	Trp	Asp	Thr	Thr	Ala	Lys	Val	
	65				70					75					80		
	Trp	Leu	Asn	Asp	Lys	Cys	Met	Met	Thr	Leu	Gln	Gly	His	Thr	Ala	Ala	
					85					90					95		
10	Val	Trp	Ala	Val	Lys	Ile	Leu	Pro	Glu	Gln	Gly	Leu	Met	Leu	Thr	Gly	
				100					105					110			
	Ser	Ala	Asp	Lys	Thr	Ile	Lys	Leu	Trp	Lys	Ala	Gly	Arg	Cys	Glu	Arg	
				115				120					125				
15	Thr	Phe	Leu	Gly	His	Glu	Asp	Cys	Val	Arg	Gly	Leu	Ala	Ile	Leu	Ser	
				130				135					140				
	Glu	Thr	Glu	Phe	Leu	Ser	Cys	Ala	Asn	Asp	Ala	Ser	Ile	Arg	Arg	Trp	
20				145			150				155					160	
	Gln	Ile	Thr	Gly	Glu	Cys	Leu	Glu	Val	Tyr	Phe	Gly	His	Thr	Asn	Tyr	
					165					170					175		
25	Ile	Tyr	Ser	Ile	Ser	Val	Phe	Pro	Asn	Ser	Lys	Asp	Phe	Val	Thr	Thr	
				180					185					190			
	Ala	Glu	Asp	Arg	Ser	Leu	Arg	Ile	Trp	Lys	His	Gly	Glu	Cys	Ala	Gln	
				195				200					205				
30	Thr	Ile	Arg	Leu	Pro	Ala	Gln	Ser	Ile	Trp	Cys	Cys	Cys	Val	Leu	Glu	
				210			215						220				
	Asn	Gly	Asp	Ile	Val	Val	Gly	Ala	Ser	Asp	Gly	Ile	Ile	Arg	Val	Phe	
35				225			230				235					240	
	Thr	Glu	Ser	Glu	Glu	Arg	Thr	Ala	Ser	Ala	Glu	Glu	Ile	Lys	Ala	Ser	
					245					250				255			
40	Leu	Ser	Arg	Glu	Ser	Pro	Leu	Ile	Ala	Lys	Val	Leu	Thr	Thr	Glu	Pro	
				260					265					270			
	Pro	Ile	Ile	Thr	Pro	Val	Arg	Arg	Thr	Leu	Pro	Cys	Arg	Val	Thr	Arg	
				275				280					285				
45	Ser	Met	Ile	Ser	Ser	Cys	Leu	Ser	Arg	Leu	Val	Ser	Thr	Ser	Leu	Ser	

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290

295

300

Thr Ser Asp Ser His Leu Thr Ile Thr Ala Leu His Leu Phe Leu Thr
 305 310 315 320

5

Thr Thr Thr Thr Glu
 325

(2) INFORMATION FOR SEQ ID NO:58:

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 425 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: unknown

15

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

20

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: RETINOBLASTOMA BINDING PROTEIN -
 HUMAN, Fig. 41

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

30

Met Ala Asp Lys Glu Ala Ala Phe Asp Asp Ala Val Glu Glu Arg Val
 1 5 10 15

Ile Asn Glu Glu Tyr Lys Ile Trp Lys Lys Asn Thr Pro Phe Leu Tyr
 20 25 30

35

Asp Leu Val Met Thr His Ala Leu Glu Trp Pro Ser Leu Thr Ala Gln
 35 40 45

Trp Leu Pro Asp Val Thr Arg Pro Glu Gly Lys Asp Phe Ser Ile His
 50 55 60

40

Arg Leu Val Leu Gly Thr His Thr Ser Asp Glu Gln Asn His Leu Val
 65 70 75 80

45

Ile Ala Ser Val Gln Leu Pro Asn Asp Asp Ala Gln Phe Asp Ala Ser
 85 90 95

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	His Tyr Asp Ser Glu Lys Gly Glu Phe Gly Gly Phe Gly Ser Val Ser	
	100	105 110
5	Gly Lys Ile Glu Ile Glu Ile Lys Ile Asn His Glu Gly Glu Val Asn	
	115	120 125
	Arg Ala Arg Tyr Met Pro Gln Asn Pro Cys Ile Ile Ala Thr Lys Thr	
	130	135 140
10	Pro Ser Ser Asp Val Leu Val Phe Asp Tyr Thr Lys His Pro Ser Lys	
	145	150 155 160
	Pro Asp Pro Ser Gly Glu Cys Asn Pro Asp Leu Arg Leu Arg Gly His	
	165	170 175
15	Gln Lys Glu Gly Tyr Gly Leu Ser Trp Asn Pro Asn Leu Ser Gly His	
	180	185 190
	Leu Leu Ser Ala Ser Asp Asp His Thr Ile Cys Leu Trp Asp Ile Ser	
20	195	200 205
	Ala Val Pro Lys Glu Gly Lys Val Val Asp Ala Lys Thr Ile Phe Thr	
	210	215 220
25	Gly His Thr Ala Val Val Glu Asp Val Ser Trp His Leu Leu His Glu	
	225	230 235 240
	Ser Leu Phe Gly Ser Val Ala Asp Asp Gln Lys Leu Met Ile Trp Asp	
	245	250 255
30	Thr Arg Ser Asn Asn Thr Ser Lys Pro Ser His Ser Val Asp Ala His	
	260	265 270
	Thr Ala Glu Val Asn Cys Leu Ser Phe Asn Pro Tyr Ser Glu Phe Ile	
35	275	280 285
	Leu Ala Thr Gly Ser Ala Asp Lys Thr Val Ala Leu Trp Asp Leu Arg	
	290	295 300
40	Asn Leu Lys Leu Lys Leu His Ser Phe Glu Ser His Lys Asp Glu Ile	
	305	310 315 320
	Phe Gln Val Gln Trp Ser Pro His Asn Glu Thr Ile Leu Ala Ser Ser	
	325	330 335
45	Gly Thr Asp Arg Arg Leu Asn Val Trp Asp Leu Ser Lys Ile Gly Glu	

350

5

10

15

20

25

(iv) ANTI-SENSE: NO

30

35

Met Phe Lys Ser Lys Thr Ser Thr Leu Ser Tyr Asp Glu Thr Pro Asn
1 5 10 15

40

Ser Asn Glu Gly Asp Arg Asn Ala Thr Pro Val Asn Pro Lys Glu Lys
20 25 30

Ser Gln Thr Lys His Leu Asn Ile Pro Gly Asp Arg Ser Arg His Ser
35 40 45

45

Ser Ile Ala Asp Ser Lys Arg Ser Ser Ser Arg Tyr Asp Gly Gly Tyr

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	50		55		60											
	Ser	Ala	Asp	Ile	Ile	Pro	Ala	Gln	Leu	Arg	Phe	Ile	Asp	Asn	Ile	Asp
	65					70					75					80
5																
	Tyr	Gly	Thr	Arg	Leu	Arg	Lys	Thr	Leu	His	Arg	Asn	Ser	Val	Val	Ser
					85				90					95		
	Asn	Gly	Tyr	Asn	Lys	Leu	Ser	Glu	Asn	Asp	Arg	Trp	Tyr	Phe	Asp	Leu
10					100				105					110		
	Phe	Asp	Arg	Lys	Tyr	Phe	Glu	Asn	Tyr	Leu	Glu	Glu	Pro	Thr	Tyr	Ile
				115				120					125			
15	Lys	Ile	Phe	Lys	Lys	Lys	Glu	Gly	Leu	Glu	Gln	Phe	Asp	Arg	Met	Phe
	130						135					140				
	Leu	Ala	Gln	Glu	Leu	Lys	Ile	Pro	Asp	Val	Tyr	Lys	Ser	Thr	Thr	Tyr
20	145				150					155						160
	Gln	Gly	Glu	Pro	Ala	Val	Ala	Asn	Ser	Glu	Leu	Phe	Lys	Asn	Ser	Ile
					165					170				175		
	Cys	Cys	Cys	Thr	Phe	Ser	His	Asp	Gly	Lys	Tyr	Met	Val	Ile	Gly	Cys
25				180				185					190			
	Lys	Asp	Gly	Ser	Leu	His	Leu	Trp	Lys	Val	Ile	Asn	Ser	Pro	Val	Lys
								200					205			
30	Arg	Ser	Glu	Met	Gly	Arg	Ser	Glu	Lys	Ser	Val	Ser	Ala	Ser	Arg	Ala
	210					215						220				
	Asn	Ser	Leu	Lys	Ile	Gln	Arg	His	Leu	Ala	Ser	Ile	Ser	Ser	His	Asn
35	225				230					235					240	
	Gly	Ser	Ile	Ser	Ser	Asn	Asp	Leu	Lys	Pro	Ser	Asp	Gln	Phe	Glu	Gly
					245				250				255			
	Pro	Ser	Lys	Gln	Leu	His	Leu	Tyr	Ala	Pro	Val	Phe	Tyr	Ser	Asp	Val
40				260				265					270			
	Phe	Arg	Val	Phe	Met	Glu	His	Ala	Leu	Asp	Ile	Leu	Asp	Ala	Asn	Trp
				275			280					285				
45	Ser	Lys	Asn	Gly	Phe	Leu	Ile	Thr	Ala	Ser	Met	Asp	Lys	Thr	Ala	Lys
	290					295						300				

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	L u Trp His Pro Glu Arg Lys Tyr Ser Leu Lys Thr Phe Val His Pro	
	305	310 315 320
5	Asp Phe Val Thr Ser Ala Ile Phe Phe Pro Asn Asp Asp Arg Phe Ile	
	325	330 335
	Ile Thr Gly Cys Leu Asp His Arg Cys Arg Leu Trp Ser Ile Leu Asp	
	340	345 350
10	Asn Glu Val Ser Tyr Ala Phe Asp Cys Lys Asp Leu Ile Thr Ser Leu	
	355	360 365
	Thr Leu Ser Pro Pro Gly Gly Glu Tyr Thr Ile Ile Gly Thr Phe Asn	
	370	375 380
15	Gly Tyr Ile Tyr Val Leu Leu Thr His Gly Leu Lys Phe Val Ser Ser	
	385	390 395 400
	Phe His Val Ser Asp Lys Ser Thr Gln Gly Thr Thr Lys Asn Ser Phe	
20	405	410 415
	His Pro Ser Ser Glu Tyr Gly Lys Val Gln His Gly Pro Arg Ile Thr	
	420	425 430
25	Gly Leu Gln Cys Phe Phe Ser Lys Val Asp Lys Asn Leu Arg Leu Ile	
	435	440 445
	Val Thr Thr Asn Asp Ser Lys Ile Gln Ile Phe Asp Leu Asn Glu Lys	
	450	455 460
30	Lys Pro Leu Glu Leu Phe Lys Gly Phe Gln Ser Gly Ser Ser Arg His	
	465	470 475 480
	Arg Gly Gln Phe Leu Met Met Lys Asn Glu Pro Val Val Phe Thr Gly	
35	485	490 495
	Ser Asp Asp His Trp Phe Tyr Thr Trp Lys Met Gln Ser Phe Asn Leu	
	500	505 510
40	Ser Ala Glu Met Asn Cys Thr Ala Pro His Arg Lys Lys Arg Leu Ser	
	515	520 525
	Gly Ser Met Ser Leu Lys Gly Leu Leu Arg Ile Val Ser Asn Lys Ser	
	530	535 540
45	Thr Asn Asp Glu Cys Leu Thr Glu Thr Ser Asn Gln Ser Ser Ser His	

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	545		550		555		560									
	Thr	Phe	Thr	Asn	Ser	Ser	Lys	Asn	Val	Leu	Gln	Thr	Gln	Thr	Val	Gly
				565				570							575	
5																
	Ser	Gln	Ala	Ile	Lys	Asn	Asn	His	Tyr	Ile	Ser	Phe	His	Ala	His	Asn
				580				585						590		
	Ser	Pro	Val	Thr	Cys	Ala	Ser	Ile	Ala	Pro	Asp	Val	Ala	Ile	Lys	Asn
10			595					600						605		
	Leu	Ser	Leu	Ser	Asn	Asp	Leu	Ile	Phe	Glu	Leu	Thr	Ser	Gln	Tyr	Phe
			610					615						620		
15	Lys	Glu	Met	Gly	Gln	Asn	Tyr	Ser	Glu	Ser	Lys	Glu	Thr	Cys	Asp	Asn
	625					630					635					640
	Lys	Pro	Asn	His	Pro	Val	Thr	Glu	Thr	Gly	Gly	Phe	Ser	Ser	Asn	Leu
						645				650					655	
20																
	Ser	Asn	Val	Val	Asn	Asn	Val	Gly	Thr	Ile	Leu	Ile	Thr	Thr	Asp	Ser
								660						665		670
	Gln	Gly	Leu	Ile	Arg	Val	Phe	Arg	Thr	Asp	Ile	Leu	Pro	Glu	Ile	Arg
25								675			680			685		
	Lys	Lys	Ile	Ile	Glu	Lys	Phe	His	Glu	Tyr	Asn	Leu	Phe	His	Leu	Glu
								690			695			700		
30	Ala	Ala	Gly	Lys	Ile	Asn	Asn	His	Asn	Asn	Asp	Ser	Ile	Leu	Glu	Asn
	705						710				715					720
	Arg	Met	Asp	Glu	Arg	Ser	Ser	Thr	Glu	Asp	Asn	Glu	Phe	Ser	Thr	Thr
							725				730					735
35																
	Pro	Pro	Ser	Asn	Thr	His	Asn	Ser	Arg	Pro	Ser	His	Asp	Phe	Cys	Glu
							740				745			750		
	Leu	His	Pro	Asn	Asn	Ser	Pro	Val	Ile	Ser	Gly	Met	Pro	Ser	Arg	Ala
40								755			760			765		
	Ser	Ala	Ile	Phe	Lys	Asn	Ser	Ile	Phe	Asn	Lys	Ser	Asn	Gly	Ser	Phe
							770				775			780		
45	Ile	Ser	Leu	Lys	Ser	Arg	Ser	Glu	Ser	Thr	Ser	Ser	Thr	Val	Phe	Gly
	785						790				795					800

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	Asn Lys Leu Ala Thr Gly Ser Ala Asp Gly Val Ile Lys Tyr Trp Asn	
	85	90 95
5	Met Ser Thr Arg Glu Glu Phe Val Ser Phe Lys Ala His Tyr Gly Leu	
	100	105 110
	Val Thr Gly Leu Cys Val Thr Gln Pro Arg Phe His Asp Lys Lys Pro	
	115	120 125
10	Asp Leu Lys Ser Gln Asn Phe Met Leu Ser Cys Ser Asp Asp Lys Thr	
	130	135 140
	Val Lys Leu Trp Ser Ile Asn Val Asp Asp Tyr Ser Asn Lys Asn Ser	
15	145	150 155 160
	Ser Asp Asn Asp Ser Val Thr Asn Glu Glu Gly Leu Ile Arg Thr Phe	
	165	170 175
20	Asp Gly Glu Ser Ala Phe Gln Gly Ile Asp Ser His Arg Glu Asn Ser	
	180	185 190
	Thr Phe Ala Thr Gly Gly Ala Lys Ile His Leu Trp Asp Val Asn Arg	
	195	200 205
25	Leu Lys Pro Val Ser Asp Leu Ser Trp Gly Ala Asp Asn Ile Thr Ser	
	210	215 220
	Leu Lys Phe Asn Gln Asn Glu Thr Asp Ile Leu Ala Ser Thr Gly Ser	
30	225	230 235 240
	Asp Asn Ser Ile Val Leu Tyr Asp Leu Arg Thr Asn Ser Pro Thr Gln	
	245	250 255
35	Lys Ile Val Gln Thr Met Arg Thr Asn Ala Ile Cys Trp Asn Pro Met	
	260	265 270
	Glu Ala Phe Asn Phe Val Thr Ala Asn Glu Asp His Asn Ala Tyr Tyr	
	275	280 285
40	Tyr Asp Met Arg Asn Leu Ser Arg Ser Leu Asn Val Phe Lys Asp His	
	290	295 300
	Val Ser Ala Val Met Asp Val Asp Phe Ser Pro Thr Gly Asp Glu Ile	
45	305	310 315 320
	Val Thr Gly Ser Tyr Asp Lys Ser Ile Arg Ile Tyr Lys Thr Asn His	

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	325		330		335
	Gly His Ser Arg Glu Ile Tyr His Thr Lys Arg Met Gln His Val Phe				
	340		345		350
5	Val Lys Tyr Ser Met Asp Ser Lys Tyr Ile Ile Ser Gly Ser Asp Asp				
	355		360		365
	Gly Asn Val Arg Leu Trp Arg Ser Lys Ala Trp Glu Arg Ser Asn Val				
10	370		375		380
	Lys Thr Thr Arg Glu Lys Asn Lys Leu Glu Tyr Asp Glu Lys Leu Lys				
	385		390		400
15	Glu Arg Phe Arg His Met Pro Glu Ile Lys Arg Ile Ser Arg His Arg				
	405		410		415
	His Val Pro Gln Val Ile Lys Lys Ala Gln Glu Ile Lys Asn Ile Glu				
20	420		425		430
	Leu Ser Ser Ile Lys Arg Arg Glu Ala Asn Glu Arg Arg Thr Arg Lys				
	435		440		445
	Asp Met Pro Tyr Ile Ser Glu Arg Lys Lys Gln Ile Val Gly Thr Val				
25	450		455		460
	His Lys Tyr Glu Asp Ser Gly Arg Asp Arg Lys Arg Arg Lys Glu Asp				
	465		470		475
30	Asp Lys Arg Asp Thr Gln Glu Lys				
	485				

(2) INFORMATION FOR SEQ ID NO:61:

- 35 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 423 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: unknown
- 40 (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- 45 (vi) ORIGINAL SOURCE:

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(C) INDIVIDUAL ISOLATE: STE4 - YEAST, Fig. 44

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

5	Met	Ala	Ala	His	Gln	Met	Asp	Ser	Ile	Thr	Tyr	Ser	Asn	Asn	Val	Thr	
	1				5					10					15		
	Gln	Gln	Tyr	Ile	Gln	Pro	Gln	Ser	Leu	Gln	Asp	Ile	Ser	Ala	Val	Glu	
10				20				25					30				
	Asp	Glu	Ile	Gln	Asn	Lys	Ile	Glu	Ala	Ala	Arg	Gln	Glu	Ser	Lys	Gln	
				35				40					45				
15	Leu	His	Ala	Gln	Ile	Asn	Lys	Ala	Lys	His	Lys	Ile	Gln	Asp	Ala	Ser	
		50					55					60					
	Leu	Phe	Gln	Met	Ala	Asn	Lys	Val	Thr	Ser	Leu	Thr	Lys	Asn	Lys	Ile	
	65					70					75				80		
20	Asn	Leu	Lys	Pro	Asn	Ile	Val	Leu	Lys	Gly	His	Asn	Asn	Lys	Ile	Ser	
					85					90					95		
	Asp	Phe	Arg	Trp	Ser	Arg	Asp	Ser	Lys	Arg	Ile	Leu	Ser	Ala	Ser	Gln	
25				100					105					110			
	Asp	Gly	Phe	Met	Leu	Ile	Trp	Asp	Ser	Ala	Ser	Gly	Leu	Lys	Gln	Asn	
				115				120					125				
30	Ala	Ile	Pro	Leu	Asp	Ser	Gln	Trp	Val	Leu	Ser	Cys	Ala	Ile	Ser	Pro	
		130					135					140					
	Ser	Ser	Thr	Leu	Val	Ala	Ser	Ala	Gly	Leu	Asn	Asn	Asn	Cys	Thr	Ile	
	145				150					155					160		
35	Tyr	Arg	Val	Ser	Lys	Glu	Asn	Arg	Val	Ala	Gln	Asn	Val	Ala	Ser	Ile	
					165					170				175			
	Phe	Lys	Gly	His	Thr	Cys	Tyr	Ile	Ser	Asp	Ile	Glu	Phe	Thr	Asp	Asn	
40				180					185					190			
	Ala	His	Ile	Leu	Thr	Ala	Ser	Gly	Asp	Met	Thr	Cys	Ala	Leu	Trp	Asp	
				195				200					205				
45	Ile	Pro	Lys	Ala	Lys	Arg	Val	Arg	Glu	Tyr	Ser	Asp	His	Leu	Gly	Asp	
		210				215						220					

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	Val	Leu	Ala	Leu	Ala	Ile	Pro	Glu	Glu	Pro	Asn	Leu	Glu	Asn	Ser	Ser	
	225					230					235					240	
5	Asn	Thr	Phe	Ala	Ser	Cys	Gly	Ser	Asp	Gly	Tyr	Thr	Tyr	Ile	Trp	Asp	
					245					250					255		
	Ser	Arg	Ser	Pro	Ser	Ala	Val	Gln	Ser	Phe	Tyr	Val	Asn	Asp	Ser	Asp	
				260					265					270			
10	Ile	Asn	Ala	Leu	Arg	Phe	Phe	Lys	Asp	Gly	Met	Ser	Ile	Val	Ala	Gly	
				275				280						285			
	Ser	Asp	Asn	Gly	Ala	Ile	Asn	Met	Tyr	Asp	Leu	Arg	Ser	Asp	Cys	Ser	
		290					295					300					
15	Ile	Ala	Thr	Phe	Ser	Leu	Phe	Arg	Gly	Tyr	Glu	Glu	Arg	Thr	Pro	Thr	
	305					310					315					320	
	Pro	Thr	Tyr	Met	Ala	Ala	Asn	Met	Glu	Tyr	Asn	Thr	Ala	Gln	Ser	Pro	
20				325					330						335		
	Gln	Thr	Leu	Lys	Ser	Thr	Ser	Ser	Ser	Tyr	Leu	Asp	Asn	Gln	Gly	Val	
				340					345					350			
25	Val	Ser	Leu	Asp	Phe	Ser	Ala	Ser	Gly	Arg	Leu	Met	Tyr	Ser	Cys	Tyr	
			355					360					365				
	Thr	Asp	Ile	Gly	Cys	Val	Val	Trp	Asp	Val	Leu	Lys	Gly	Glu	Ile	Val	
		370					375					380					
30	Gly	Lys	Leu	Glu	Gly	His	Gly	Gly	Arg	Val	Thr	Gly	Val	Arg	Ser	Ser	
	385					390					395					400	
	Pro	Asp	Gly	Leu	Ala	Val	Cys	Thr	Gly	Ser	Trp	Asp	Ser	Thr	Met	Lys	
35				405					410					415			
	Ile	Trp	Ser	Pro	Gly	Tyr	Gln										
				420													

40

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 704 amino acids

45

(B) TYPE: amino acid

(D) TOPOLOGY: unknown

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(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

5 (iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: TRANSCRIPTION FACTOR TIIF, Fig. 45

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

Met Ser Leu Glu Val Ser Asn Ile Asn Gly Gly Asn Gly Thr Gln Leu
 1 5 10 15

Ser His Asp Lys Arg Glu Leu Leu Cys Leu Leu Lys Leu Ile Lys Lys
 20 25 30

Tyr Gln Leu Lys Ser Thr Glu Glu Leu Leu Cys Gln Glu Ala Asn Val
 35 40 45

Ser Ser Val Glu Leu Ser Glu Ile Ser Glu Ser Asp Val Gln Gln Val
 50 55 60

Leu Gly Ala Val Leu Gly Ala Gly Asp Ala Asn Arg Glu Arg Lys His
 65 70 75 80

Val Gln Ser Pro Ala Gln Gly His Lys Gln Ser Ala Val Thr Glu Ala
 85 90 95

Asn Ala Ala Glu Glu Leu Ala Lys Phe Ile Asp Asp Asp Ser Phe Asp
 100 105 110

Ala Gln His Tyr Glu Gln Ala Tyr Lys Glu Leu Arg Thr Phe Val Glu
 115 120 125

Asp Ser Leu Asp Ile Tyr Lys His Glu Leu Ser Met Val Leu Tyr Pro
 130 135 140

Ile Leu Val Gln Ile Tyr Phe Lys Ile Leu Ala Ser Gly Leu Arg Glu
 145 150 155 160

Lys Ala Lys Glu Phe Ile Glu Lys Tyr Lys Cys Asp Leu Asp Gly Tyr
 165 170 175

45

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	Tyr	Ile	Glu	Gly	Leu	Phe	Asn	Leu	Leu	Leu	Leu	Ser	Lys	Pro	Glu	Glu	
					180				185					190			
5	Leu	Leu	Glu	Asn	Asp	Leu	Val	Val	Ala	Met	Glu	Gln	Asp	Lys	Phe	Val	
			195				200						205				
	Ile	Arg	Met	Ser	Arg	Asp	Ser	His	Ser	Leu	Phe	Lys	Arg	His	Ile	Gln	
			210				215					220					
10	Asp	Arg	Arg	Gln	Glu	Val	Val	Ala	Asp	Ile	Val	Ser	Lys	Tyr	Leu	His	
			225			230					235					240	
	Phe	Asp	Thr	Tyr	Glu	Gly	Met	Ala	Arg	Asn	Lys	Leu	Gln	Cys	Val	Ala	
15					245				250					255			
	Thr	Ala	Gly	Ser	His	Leu	Gly	Glu	Ala	Lys	Arg	Gln	Asp	Asn	Lys	Met	
				260					265					270			
20	Arg	Val	Tyr	Tyr	Gly	Leu	Leu	Lys	Glu	Val	Asp	Phe	Gln	Thr	Leu	Thr	
			275				280						285				
	Thr	Pro	Ala	Pro	Ala	Pro	Glu	Glu	Glu	Asp	Asp	Asp	Pro	Asp	Ala	Pro	
			290				295					300					
25	Asp	Arg	Pro	Lys	Lys	Lys	Lys	Pro	Lys	Lys	Asp	Pro	Leu	Leu	Ser	Lys	
			305			310					315					320	
	Lys	Ser	Lys	Ser	Asp	Pro	Asn	Ala	Pro	Ser	Ile	Asp	Arg	Ile	Pro	Leu	
30					325				330					335			
	Pro	Glu	Leu	Lys	Asp	Ser	Asp	Lys	Leu	Leu	Lys	Leu	Lys	Ala	Leu	Arg	
				340					345					350			
35	Glu	Ala	Ser	Lys	Arg	Leu	Ala	Leu	Ser	Lys	Asp	Gln	Leu	Pro	Ser	Ala	
			355				360					365					
	Val	Phe	Tyr	Thr	Val	Leu	Asn	Ser	His	Gln	Gly	Val	Thr	Cys	Ala	Glu	
			370				375					380					
40	Ile	Ser	Asp	Asp	Ser	Thr	Met	Leu	Ala	Cys	Gly	Phe	Gly	Asp	Ser	Ser	
			385			390					395					400	
	Val	Arg	Ile	Trp	Ser	Leu	Thr	Pro	Ala	Asn	Val	Arg	Thr	Leu	Lys	Asp	
45				405					410					415			
	Ala	Asp	Ser	Leu	Arg	Glu	Leu	Asp	Lys	Glu	Ser	Ala	Asp	Ile	Asn	Val	

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	420	425	430
	Arg Met Leu Asp Asp Arg Ser Gly Glu Val Thr Arg Ser Leu Met Gly		
	435	440	445
5	His Thr Gly Pro Val Tyr Arg Cys Ala Phe Ala Pro Glu Met Asn Leu		
	450	455	460
	Leu Leu Ser Cys Ser Glu Asp Ser Thr Ile Arg Leu Trp Ser Leu Leu		
10	465	470	475 480
	Thr Trp Ser Cys Val Val Thr Tyr Arg Gly His Val Tyr Pro Val Trp		
	485	490	495
15	Asp Val Arg Phe Ala Pro His Gly Tyr Tyr Phe Val Ser Cys Ser Tyr		
	500	505	510
	Asp Lys Thr Ala Arg Leu Trp Ala Thr Asp Ser Asn Gln Ala Leu Arg		
	515	520	525
20	Val Phe Val Gly His Leu Ser Asp Val Asp Cys Val Gln Phe His Pro		
	530	535	540
	Asn Ser Asn Tyr Val Ala Thr Gly Ser Ser Asp Arg Thr Val Arg Leu		
25	545	550	555 560
	Trp Asp Asn Met Thr Gly Gln Ser Val Arg Leu Met Thr Gly His Lys		
	565	570	575
30	Gly Ser Val Ser Ser Leu Ala Phe Ser Ala Cys Gly Arg Tyr Leu Ala		
	580	585	590
	Ser Gly Ser Val Asp His Asn Ile Ile Ile Trp Asp Leu Ser Asn Gly		
	595	600	605
35	Ser Leu Val Thr Thr Leu Leu Arg His Thr Ser Thr Val Thr Thr Ile		
	610	615	620
	Thr Phe Ser Arg Asp Gly Thr Val Leu Ala Ala Ala Gly Leu Asp Asn		
40	625	630	635 640
	Asn Leu Thr Leu Trp Asp Phe His Lys Val Thr Glu Asp Tyr Ile Ser		
	645	650	655
45	Asn His Ile Thr Val Ser His His Gln Asp Glu Asn Asp Glu Asp Val		
	660	665	670

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	Gln Gln Gln Gln Gln Gln Leu Ala Ala Ala Ser Ala Ser Val Pro Val	
	115	120 125
5	Ala Gln Gln Pro Pro Ala Thr Thr Ser Ala Thr Ala Thr Pro Ala Ala	
	130	135 140
	Asn Thr Thr Thr Gly Ser Pro Ser Ala Phe Pro Val Gln Ala Ser Arg	
	145	150 155 160
10	Pro Asn Leu Val Gly Ser Gln Leu Pro Thr Thr Thr Leu Pro Val Val	
	165	170 175
	Ser Ser Asn Ala Gln Gln Gln Leu Pro Gln Gln Gln Leu Gln Gln Gln	
15	180	185 190
	Gln Leu Gln Gln Gln Gln Pro Pro Pro Gln Val Ser Val Ala Pro Leu	
	195	200 205
	Ser Asn Thr Ala Ile Asn Gly Ser Pro Thr Ser Lys Glu Thr Thr Thr	
20	210	215 220
	Leu Pro Ser Val Lys Ala Pro Glu Ser Thr Leu Lys Glu Thr Glu Pro	
	225	230 235 240
25	Glu Asn Asn Asn Thr Ser Lys Ile Asn Asp Thr Gly Ser Ala Thr Thr	
	245	250 255
	Ala Thr Thr Thr Thr Ala Thr Glu Thr Glu Ile Lys Pro Lys Glu Glu	
30	260	265 270
	Asp Ala Thr Pro Ala Ser Leu His Gln Asp His Tyr Leu Val Pro Tyr	
	275	280 285
35	Asn Gln Arg Ala Asn His Ser Lys Pro Ile Pro Pro Phe Leu Leu Asp	
	290	295 300
	Leu Asp Ser Gln Ser Val Pro Asp Ala Leu Lys Lys Gln Thr Asn Asp	
	305	310 315 320
40	Tyr Tyr Ile Leu Tyr Asn Pro Ala Leu Pro Arg Glu Ile Asp Val Glu	
	325	330 335
	Leu His Lys Ser Leu Asp His Thr Ser Val Val Cys Cys Val Lys Phe	
45	340	345 350
	Ser Asn Asp Gly Glu Tyr Leu Ala Thr Gly Cys Asn Lys Thr Thr Gln	

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	355	360	365
	Val Tyr Arg Val Ser Asp Gly Ser Leu Val Ala Arg Leu Ser Asp Asp		
	370	375	380
5	Ser Ala Ala Asn Asn His Arg Asn Ser Ile Thr Glu Asn Asn Thr Thr		
	385	390	395 400
	Thr Ser Thr Asp Asn Asn Thr Met Thr Thr Thr Thr Thr Thr Thr Ile		
10		405	410 415
	Thr Thr Thr Ala Met Thr Ser Ala Ala Glu Leu Ala Lys Asp Val Glu		
		420	425 430
15	Asn Leu Asn Thr Ser Ser Ser Pro Ser Ser Asp Leu Tyr Ile Arg Ser		
	435	440	445
	Val Cys Phe Ser Pro Asp Gly Lys Phe Leu Ala Thr Gly Ala Glu Asp		
	450	455	460
20	Arg Leu Ile Arg Ile Trp Asp Ile Glu Asn Arg Lys Ile Val Met Ile		
	465	470	475 480
	Leu Gln Gly His Glu Gln Asp Ile Tyr Ser Leu Asp Tyr Phe Pro Ser		
25		485	490 495
	Gly Asp Lys Leu Val Ser Gly Ser Gly Asp Arg Thr Val Arg Ile Trp		
		500	505 510
30	Asp Leu Arg Thr Gly Gln Cys Ser Leu Thr Leu Ser Ile Glu Asp Gly		
	515	520	525
	Val Thr Thr Val Ala Val Ser Pro Gly Asp Gly Lys Tyr Ile Ala Ala		
	530	535	540
35	Gly Ser Leu Asp Arg Ala Val Arg Val Trp Asp Ser Glu Thr Gly Phe		
	545	550	555 560
	Leu Val Glu Arg Leu Asp Ser Glu Asn Glu Ser Gly Thr Gly His Lys		
40		565	570 575
	Asp Ser Val Tyr Ser Val Val Phe Thr Arg Asp Gly Gln Ser Val Val		
	580	585	590
45	Ser Gly Ser Leu Asp Arg Ser Val Lys Leu Trp Asn Leu Gln Asn Ala		
	595	600	605

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	Asn	Asn	Lys	Ser	Asp	Ser	Lys	Thr	Pro	Asn	Ser	Gly	Thr	Cys	Glu	Val
	610						615					620				
5	Thr	Tyr	Ile	Gly	His	Lys	Asp	Phe	Val	Leu	Ser	Val	Ala	Thr	Thr	Gln
	625					630					635					640
	Asn	Asp	Glu	Tyr	Ile	Leu	Ser	Gly	Ser	Lys	Asp	Arg	Gly	Val	Leu	Phe
					645					650					655	
10	Trp	Asp	Lys	Lys	Ser	Gly	Asn	Pro	Leu	Leu	Met	Leu	Gln	Gly	His	Arg
			660					665					670			
	Asn	Ser	Val	Ile	Ser	Val	Ala	Val	Ala	Asn	Gly	Ser	Ser	Leu	Gly	Pro
15			675					680					685			
	Glu	Tyr	Asn	Val	Phe	Ala	Thr	Gly	Ser	Gly	Asp	Cys	Lys	Ala	Arg	Ile
		690					695				700					
	Trp	Lys	Tyr	Lys	Lys	Ile	Ala	Pro	Asn							
20	705					710										

(2) INFORMATION FOR SEQ ID NO:64:

- (i) SEQUENCE CHARACTERISTICS:
- 25 (A) LENGTH: 798 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: protein
- 30 (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- 35 (vi) ORIGINAL SOURCE:
- (C) INDIVIDUAL ISOLATE: TUP1 HOMOLOG, Fig. 47

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

40 Met Ser Gln Lys Gln Ser Thr Asn Gln Asn Gln Asn Gly Thr His Gln

1 5 10 15

Pro Gln Pro Val Lys Asn Gln Arg Thr Asn Asn Ala Ala Gly Ala Asn

45 20 25 30

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	Ser Gly Gln Gln Pro Gln Gln Gln Ser Gln Gly Gln Ser Gln Gln Gln
	35 40 45
5	Gly Arg Ser Asn Gly Pro Phe Ser Ala Ser Asp Leu Asn Arg Ile Val
	50 55 60
	Leu Glu Tyr Leu Asn Lys Lys Gly Tyr His Arg Thr Glu Ala Met Leu
	65 70 75 80
10	Arg Ala Glu Ser Gly Arg Thr Leu Thr Pro Gln Asn Lys Gln Ser Pro
	85 90 95
	Ala Asn Thr Lys Thr Gly Lys Phe Pro Glu Gln Ser Ser Ile Pro Pro
	100 105 110
15	Asn Pro Gly Lys Thr Ala Lys Pro Ile Ser Asn Pro Thr Asn Leu Ser
	115 120 125
	Ser Lys Arg Asp Ala Glu Gly Gly Ile Val Ser Ser Gly Arg Leu Glu
20	130 135 140
	Gly Leu Asn Ala Pro Glu Asn Tyr Ile Arg Ala Tyr Ser Met Leu Lys
	145 150 155 160
25	Asn Trp Val Asp Ser Ser Leu Glu Ile Tyr Lys Pro Glu Leu Ser Tyr
	165 170 175
	Ile Met Tyr Pro Ile Phe Ile Tyr Leu Phe Leu Asn Leu Val Ala Lys
	180 185 190
30	Asn Pro Val Tyr Ala Arg Arg Phe Phe Asp Arg Phe Ser Pro Asp Phe
	195 200 205
	Lys Asp Phe His Gly Ser Glu Ile Asn Arg Leu Phe Ser Val Asn Ser
35	210 215 220
	Ile Asp His Ile Lys Glu Asn Glu Val Ala Ser Ala Phe Gln Ser His
	225 230 235 240
40	Lys Tyr Arg Ile Thr Met Ser Lys Thr Thr Leu Asn Leu Leu Leu Tyr
	245 250 255
	Phe Leu Asn Glu Asn Glu Ser Ile Gly Gly Ser Leu Ile Ile Ser Val
	260 265 270
45	Ile Asn Gln His Leu Asp Pro Asn Ile Val Glu Ser Val Thr Ala Arg

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	275		280		285
	Glu Lys Leu Ala Asp Gly Ile Lys Val Leu Ser Asp Ser Glu Asn Gly				
	290		295		300
5	Asn Gly Lys Gln Asn Leu Glu Met Asn Ser Val Pro Val Lys Leu Gly				
	305		310		315 320
	Pro Phe Pro Lys Asp Glu Glu Phe Val Lys Glu Ile Glu Thr Glu Leu				
10		325		330	335
	Lys Ile Lys Asp Asp Gln Glu Lys Gln Leu Asn Gln Gln Thr Ala Gly				
		340		345	350
15	Asp Asn Tyr Ser Gly Ala Asn Asn Arg Thr Leu Leu Gln Glu Tyr Lys				
		355		360	365
	Ala Met Asn Asn Glu Lys Phe Lys Asp Asn Thr Gly Asp Asp Asp Lys				
20		370		375	380
	Asp Lys Ile Lys Asp Lys Ile Ala Lys Asp Glu Glu Lys Lys Glu Ser				
	385		390		395 400
	Glu Leu Lys Val Asp Gly Glu Lys Lys Asp Ser Asn Leu Ser Ser Pro				
25		405		410	415
	Ala Arg Asp Ile Leu Pro Leu Pro Pro Lys Thr Ala Leu Asp Leu Lys				
		420		425	430
30	Leu Glu Ile Gln Lys Val Lys Glu Ser Arg Asp Ala Ile Lys Leu Asp				
		435		440	445
	Asn Leu Gln Leu Ala Leu Pro Ser Val Cys Met Tyr Thr Phe Gln Asn				
35		450		455	460
	Thr Asn Lys Asp Met Ser Cys Leu Asp Phe Ser Asp Asp Cys Arg Ile				
	465		470		475 480
	Ala Ala Ala Gly Phe Gln Asp Ser Tyr Ile Lys Ile Trp Ser Leu Asp				
40		485		490	495
	Gly Ser Ser Leu Asn Asn Pro Asn Ile Ala Leu Asn Asn Asn Asp Lys				
		500		505	510
45	Asp Glu Asp Pro Thr Cys Lys Thr Leu Val Gly His Ser Gly Thr Val				
		515		520	525

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	Tyr Ser Thr Ser Phe Ser Pro Asp Asn Lys Tyr Leu Leu Ser Gly Ser	
	530	540
5	Glu Asp Lys Thr Val Arg Leu Trp Ser Met Asp Thr His Thr Ala Leu	
	545	550 555 560
	Val Ser Tyr Lys Gly His Asn His Pro Val Trp Asp Val Ser Phe Ser	
		565 570 575
10	Pro Leu Gly His Tyr Phe Ala Thr Ala Ser His Asp Gln Thr Ala Arg	
		580 585 590
	Leu Trp Ser Cys Asp His Ile Tyr Pro Leu Arg Ile Phe Ala Gly His	
		595 600 605
15	Leu Asn Asp Val Asp Cys Val Ser Phe His Pro Asn Gly Cys Tyr Val	
		610 615 620
	Phe Thr Gly Ser Ser Asp Lys Thr Cys Arg Met Trp Asp Val Ser Thr	
20		625 630 635 640
	Gly Asp Ser Val Arg Leu Phe Leu Gly His Thr Ala Pro Val Ile Ser	
		645 650 655
25	Ile Ala Val Cys Pro Asp Gly Arg Trp Leu Ser Thr Gly Ser Glu Asp	
		660 665 670
	Gly Ile Ile Asn Val Trp Asp Ile Gly Thr Gly Lys Arg Leu Lys Gln	
		675 680 685
30	Met Arg Gly His Gly Lys Asn Ala Ile Tyr Ser Leu Ser Tyr Ser Lys	
		690 695 700
	Glu Gly Asn Val Leu Ile Ser Gly Gly Ala Asp His Thr Val Arg Val	
35		705 710 715 720
	Trp Asp Leu Lys Lys Ala Thr Thr Glu Pro Ser Ala Glu Pro Asp Glu	
		725 730 735
40	Pro Phe Ile Gly Tyr Leu Gly Asp Val Thr Ala Ser Ile Asn Gln Asp	
		740 745 750
	Ile Lys Glu Tyr Gly Arg Arg Arg Thr Val Ile Pro Thr Ser Asp Leu	
		755 760 765
45	Val Ala Ser Phe Tyr Thr Lys Lys Thr Pro Val Phe Lys Val Lys Phe	

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770

775

780

Ser Arg Ser Asn Leu Ala Leu Ala Gly Gly Ala Phe Arg Pro

785

790

795

5

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 439 amino acids

10

(B) TYPE: amino acid

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

15

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

20

(C) INDIVIDUAL ISOLATE: YCU7, Fig. 48

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

25

Met Val Arg Arg Phe Arg Gly Lys Glu Leu Ala Ala Thr Thr Phe Asn

1

5

10

15

Gly His Arg Asp Tyr Val Met Gly Ala Phe Phe Ser His Asp Gln Glu

20

25

30

30

Lys Ile Tyr Thr Val Ser Lys Asp Gly Ala Val Phe Val Trp Glu Phe

35

40

45

Thr Lys Arg Pro Ser Asp Asp Asp Asn Glu Ser Glu Asp Asp Asp

35

50

55

60

Lys Gln Glu Glu Val Asp Ile Ser Lys Tyr Ser Trp Arg Ile Thr Lys

65

70

75

80

40

Lys His Phe Phe Tyr Ala Asn Gln Ala Lys Val Lys Cys Val Thr Phe

85

90

95

His Pro Ala Thr Arg Leu Leu Ala Val Gly Phe Thr Ser Gly Glu Phe

100

105

110

45

Arg Leu Tyr Asp Leu Pro Asp Phe Thr Leu Ile Gln Gln Leu Ser Met

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	115	120	125
	Gly Gln Asn Pro Val Asn Thr Val Ser Val Asn Gln Thr Gly Glu Trp		
	130	135	140
5	Leu Ala Phe Gly Ser Ser Lys Leu Gly Gln Leu Leu Val Tyr Glu Trp		
	145	150	155 160
	Gln Ser Glu Ser Tyr Ile Leu Lys Gln Gln Gly His Phe Asp Ser Thr		
10	165	170	175
	Asn Ser Leu Ala Tyr Ser Pro Asp Gly Ser Arg Val Val Thr Ala Ser		
	180	185	190
15	Glu Asp Gly Lys Ile Lys Val Trp Asp Ile Thr Ser Gly Phe Cys Leu		
	195	200	205
	Ala Thr Phe Glu Glu His Thr Ser Ser Val Thr Ala Val Gln Phe Ala		
	210	215	220
20	Lys Arg Gly Gln Val Met Phe Ser Ser Ser Leu Asp Gly Thr Val Arg		
	225	230	235 240
	Ala Trp Asp Leu Ile Arg Tyr Arg Asn Phe Arg Thr Phe Thr Gly Thr		
25	245	250	255
	Glu Arg Ile Gln Phe Asn Cys Leu Ala Val Asp Pro Ser Gly Glu Val		
	260	265	270
30	Val Cys Ala Gly Ser Leu Asp Asn Phe Asp Ile His Val Trp Ser Val		
	275	280	285
	Gln Thr Gly Gln Leu Leu Asp Ala Leu Ser Gly His Glu Gly Pro Val		
	290	295	300
35	Ser Cys Leu Ser Phe Ser Gln Glu Asn Ser Val Leu Ala Ser Ala Ser		
	305	310	315 320
	Trp Asp Lys Thr Ile Arg Ile Trp Ser Ile Phe Gly Arg Ser Gln Gln		
40	325	330	335
	Val Glu Pro Ile Glu Val Tyr Ser Asp Val Leu Ala Leu Ser Met Arg		
	340	345	350
45	Pro Asp Gly Lys Glu Val Ala Val Ser Thr Leu Lys Gly Gln Ile Ser		
	355	360	365

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Ile Phe Asn Ile Glu Asp Ala Lys Gln Val Gly Asn Ile Asp Cys Arg
 370 375 380

Lys Asp Ile Ile Ser Gly Arg Phe Asn Gln Asp Arg Phe Thr Ala Lys
 5 385 390 395 400

Ile Leu Asn Asp Pro Asn Phe Leu Leu Gln Tyr Ile Thr Val Leu Met
 405 410 415

Val Trp Leu Leu Trp Leu Val Val Ile Ile Thr Pro Phe Val Tyr Met
 10 420 425 430

Met Phe Gln Met Lys Ser Cys
 435

15

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 514 amino acids
 20 (B) TYPE: amino acid
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

25 (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

30 (C) INDIVIDUAL ISOLATE: YCW2 PROTEIN, Fig. 49

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

Met Ser Thr Leu Ile Pro Pro Pro Ser Lys Lys Gln Lys Lys Glu Ala
 1 5 10 15

Gln Leu Pro Arg Glu Val Ala Ile Ile Pro Lys Asp Leu Pro Asn Val
 20 25 30

Ser Ile Lys Phe Gln Ala Leu Asp Thr Gly Asp Asn Val Gly Gly Ala
 35 40 45

Leu Arg Val Pro Gly Ala Ile Ser Glu Lys Gln Leu Glu Glu Leu Leu
 45 50 55 60

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	Asn Gln Leu Asn Gly Thr Ser Asp Asp Pro Val Pro Tyr Thr Phe Ser	
	65	70 75 80
5	Cys Thr Ile Gln Gly Lys Lys Ala Ser Asp Pro Val Lys Thr Ile Asp	
		85 90 95
	Ile Thr Asp Asn Leu Tyr Ser Ser Leu Ile Lys Pro Gly Tyr Asn Ser	
		100 105 110
10	Thr Glu Asp Gln Ile Thr Leu Leu Tyr Thr Pro Arg Ala Val Phe Lys	
		115 120 125
	Val Lys Pro Val Thr Arg Ser Ser Ser Ala Ile Ala Gly His Gly Ser	
		130 135 140
15	Thr Ile Leu Cys Ser Ala Phe Ala Pro His Thr Ser Ser Arg Met Val	
		145 150 155 160
	Thr Gly Ala Gly Asp Asn Thr Ala Arg Ile Trp Asp Cys Asp Thr Gln	
20		165 170 175
	Thr Pro Met His Thr Leu Lys Gly His Tyr Asn Trp Val Leu Cys Val	
		180 185 190
25	Ser Trp Ser Pro Asp Gly Glu Val Ile Ala Thr Gly Ser Met Asp Asn	
		195 200 205
	Thr Ile Arg Leu Trp Asp Pro Lys Ser Gly Gln Cys Leu Gly Asp Ala	
		210 215 220
30	Leu Arg Gly His Ser Lys Trp Ile Thr Ser Leu Ser Trp Glu Pro Ile	
		225 230 235 240
	His Leu Val Lys Pro Gly Ser Lys Pro Arg Leu Ala Ser Ser Ser Lys	
35		245 250 255
	Asp Gly Thr Ile Lys Ile Trp Asp Thr Val Ser Arg Val Cys Gln Tyr	
		260 265 270
40	Thr Met Ser Gly His Thr Asn Ser Val Ser Cys Val Lys Trp Gly Gly	
		275 280 285
	Gln Gly Leu Leu Tyr Ser Gly Ser His Asp Arg Thr Val Arg Val Trp	
		290 295 300
45	Asp Ile Asn Ser Gln Gly Arg Cys Ile Asn Ile Leu Lys Ser His Ala	

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	305		310		315		320
	His Trp Val Asn His Leu Ser Leu Ser Thr Asp Tyr Ala Leu Arg Ile						
		325		330		335	
5							
	Gly Ala Phe Asp His Thr Gly Lys Lys Pro Ser Thr Pro Glu Glu Ala						
		340		345		350	
	Gln Lys Lys Ala Leu Glu Asn Tyr Glu Lys Ile Cys Lys Lys Asn Gly						
10		355		360		365	
	Asn Ser Glu Glu Met Met Val Thr Ala Ser Asp Asp Tyr Thr Met Phe						
		370		375		380	
15							
	Leu Trp Asn Pro Leu Lys Ser Thr Lys Pro Ile Ala Arg Met Thr Gly						
		385		390		395	400
	His Gln Lys Leu Val Asn His Val Ala Phe Ser Pro Asp Gly Arg Tyr						
		405		410		415	
20							
	Ile Val Ser Ala Ser Phe Asp Asn Ser Ile Lys Leu Trp Asp Gly Arg						
		420		425		430	
	Asp Gly Lys Phe Ile Ser Thr Phe Arg Gly His Ile Ala Ser Val Tyr						
25		435		440		445	
	Gln Val Ala Trp Ser Ser Asp Cys Arg Leu Leu Val Ser Cys Ser Lys						
		450		455		460	
30							
	Asp Thr Thr Leu Lys Val Trp Asp Val Arg Thr Arg Lys Leu Ser Val						
		465		470		475	480
	Asp Leu Pro Gly Ile Lys Thr Lys Leu Tyr Val Asp Trp Ser Val Asp						
		485		490		495	
35							
	Gly Lys Arg Val Cys Ser Gly Gly Lys Asp Lys Met Val Arg Leu Trp						
		500		505		510	
	Thr His						
40							

(2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 852 amino acids
(B) TYPE: amino acid

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(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

5 (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

10 (C) INDIVIDUAL ISOLATE: YKL525, Fig. 50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

```

15 Met Phe Lys Ser Lys Thr Ser Thr Leu Ser Tyr Asp Glu Thr Pro Asn
   1             5             10             15

Ser Asn Glu Gly Asp Arg Asn Ala Thr Pro Val Asn Pro Lys Glu Lys
           20             25             30

20 Ser Gln Thr Lys His Leu Asn Ile Pro Gly Asp Arg Ser Arg His Ser
           35             40             45

Ser Ile Ala Asp Ser Lys Arg Ser Ser Ser Arg Tyr Asp Gly Gly Tyr
25           50             55             60

Ser Ala Asp Ile Ile Pro Ala Gln Leu Arg Phe Ile Asp Asn Ile Asp
           65             70             75             80

30 Tyr Gly Thr Arg Leu Arg Lys Thr Leu His Arg Asn Ser Val Val Ser
           85             90             95

Asn Gly Tyr Asn Lys Leu Ser Glu Asn Asp Arg Trp Tyr Phe Asp Leu
           100            105            110

35 Phe Asp Arg Lys Tyr Phe Glu Asn Tyr Leu Glu Glu Pro Thr Tyr Ile
           115            120            125

Lys Ile Phe Lys Lys Lys Glu Gly Leu Glu Gln Phe Asp Arg Met Phe
40           130            135            140

Leu Ala Gln Glu Leu Lys Ile Pro Asp Val Tyr Lys Ser Thr Thr Tyr
           145            150            155            160

45 Gln Gly Glu Pro Ala Val Ala Asn Ser Glu Leu Phe Lys Asn Ser Ile
           165            170            175

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	Cys Cys Cys Thr Phe Ser His Asp Gly Lys Tyr Met Val Ile Gly Cys	
	180	185 190
5	Lys Asp Gly Ser Leu His Leu Trp Lys Val Ile Asn Ser Pro Val Lys	
	195	200 205
	Arg Ser Glu Met Gly Arg Ser Glu Lys Ser Val Ser Ala Ser Arg Ala	
	210	215 220
10	Asn Ser Leu Lys Ile Gln Arg His Leu Ala Ser Ile Ser Ser His Asn	
	225	230 235 240
	Gly Ser Ile Ser Ser Asn Asp Leu Lys Pro Ser Asp Gln Phe Glu Gly	
	245	250 255
15	Pro Ser Lys Gln Leu His Leu Tyr Ala Pro Val Phe Tyr Ser Asp Val	
	260	265 270
	Phe Arg Val Phe Met Glu His Ala Leu Asp Ile Leu Asp Ala Asn Trp	
20	275	280 285
	Ser Lys Asn Gly Phe Leu Ile Thr Ala Ser Met Asp Lys Thr Ala Lys	
	290	295 300
25	Leu Trp His Pro Glu Arg Lys Tyr Ser Leu Lys Thr Phe Val His Pro	
	305	310 315 320
	Asp Phe Val Thr Ser Ala Ile Phe Phe Pro Asn Asp Asp Arg Phe Ile	
	325	330 335
30	Ile Thr Gly Cys Leu Asp His Arg Cys Arg Leu Trp Ser Ile Leu Asp	
	340	345 350
	Asn Glu Val Ser Tyr Ala Phe Asp Cys Lys Asp Leu Ile Thr Ser Leu	
35	355	360 365
	Thr Leu Ser Pro Pro Gly Gly Glu Tyr Thr Ile Ile Gly Thr Phe Asn	
	370	375 380
40	Gly Tyr Ile Tyr Val Leu Leu Thr His Gly Leu Lys Phe Val Ser Ser	
	385	390 395 400
	Phe His Val Ser Asp Lys Ser Thr Gln Gly Thr Thr Lys Asn Ser Phe	
	405	410 415
45	His Pro Ser Ser Glu Tyr Gly Lys Val Gln His Gly Pro Arg Ile Thr	

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	420	425	430
	Gly Leu Gln Cys Phe Phe Ser Lys Val Asp Lys Asn Leu Arg Leu Ile		
	435	440	445
5	Val Thr Thr Asn Asp Ser Lys Ile Gln Ile Phe Asp Leu Asn Glu Lys		
	450	455	460
10	Lys Pro Leu Glu Leu Phe Lys Gly Phe Gln Ser Gly Ser Ser Arg His		
	465	470	475 480
	Arg Gly Gln Phe Leu Met Met Lys Asn Glu Pro Val Val Phe Thr Gly		
	485	490	495
15	Ser Asp Asp His Trp Phe Tyr Thr Trp Lys Met Gln Ser Phe Asn Leu		
	500	505	510
	Ser Ala Glu Met Asn Cys Thr Ala Pro His Arg Lys Lys Arg Leu Ser		
	515	520	525
20	Gly Ser Met Ser Leu Lys Gly Leu Leu Arg Ile Val Ser Asn Lys Ser		
	530	535	540
	Thr Asn Asp Glu Cys Leu Thr Glu Thr Ser Asn Gln Ser Ser Ser His		
25	545	550	555 560
	Thr Phe Thr Asn Ser Ser Lys Asn Val Leu Gln Thr Gln Thr Val Gly		
	565	570	575
30	Ser Gln Ala Ile Lys Asn Asn His Tyr Ile Ser Phe His Ala His Asn		
	580	585	590
	Ser Pro Val Thr Cys Ala Ser Ile Ala Pro Asp Val Ala Ile Lys Asn		
	595	600	605
35	Leu Ser Leu Ser Asn Asp Leu Ile Phe Glu Leu Thr Ser Gln Tyr Phe		
	610	615	620
	Lys Glu Met Gly Gln Asn Tyr Ser Glu Ser Lys Glu Thr Cys Asp Asn		
40	625	630	635 640
	Lys Pro Asn His Pro Val Thr Glu Thr Gly Gly Phe Ser Ser Asn Leu		
	645	650	655
45	Ser Asn Val Val Asn Asn Val Gly Thr Ile Leu Ile Thr Thr Asp Ser		
	660	665	670

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	Gln Gly Leu Ile Arg Val Phe Arg Thr Asp Ile Leu Pro Glu Ile Arg	
	675	680 685
5	Lys Lys Ile Ile Glu Lys Phe His Glu Tyr Asn Leu Phe His Leu Glu	
	690	695 700
	Ala Ala Gly Lys Ile Asn Asn His Asn Asn Asp Ser Ile Leu Glu Asn	
	705	710 715 720
10	Arg Met Asp Glu Arg Ser Ser Thr Glu Asp Asn Glu Phe Ser Thr Thr	
	725	730 735
	Pro Pro Ser Asn Thr His Asn Ser Arg Pro Ser His Asp Phe Cys Glu	
	740	745 750
15	Leu His Pro Asn Asn Ser Pro Val Ile Ser Gly Met Pro Ser Arg Ala	
	755	760 765
	Ser Ala Ile Phe Lys Asn Ser Ile Phe Asn Lys Ser Asn Gly Ser Phe	
20	770	775 780
	Ile Ser Leu Lys Ser Arg Ser Glu Ser Thr Ser Ser Thr Val Phe Gly	
	785	790 795 800
25	Pro His Asp Ile Pro Arg Val Ser Thr Thr Tyr Pro Lys Leu Lys Cys	
	805	810 815
	Asp Val Cys Asn Gly Ser Asn Phe Glu Cys Ala Ser Lys Asn Pro Ile	
	820	825 830
30	Ala Gly Gly Asp Ser Gly Phe Thr Cys Ala Asp Cys Gly Thr Ile Leu	
	835	840 845
	Asn Asn Phe Arg	
35	850	

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 798 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

45

(iii) HYPOTHETICAL: NO

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(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: yrb 1410 yeast, Fig. 51

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

10	Met Ser Gln Lys Gln Ser Thr Asn Gln Asn Gln Asn Gly Thr His Gln	1	5	10	15
	Pro Gln Pro Val Lys Asn Gln Arg Thr Asn Asn Ala Ala Gly Ala Asn	20	25	30	
15	Ser Gly Gln Gln Pro Gln Gln Gln Ser Gln Gly Gln Ser Gln Gln Gln	35	40	45	
	Gly Arg Ser Asn Gly Pro Phe Ser Ala Ser Asp Leu Asn Arg Ile Val	50	55	60	
20	Leu Glu Tyr Leu Asn Lys Lys Gly Tyr His Arg Thr Glu Ala Met Leu	65	70	75	80
	Arg Ala Glu Ser Gly Arg Thr Leu Thr Pro Gln Asn Lys Gln Ser Pro	85	90	95	
	Ala Asn Thr Lys Thr Gly Lys Phe Pro Glu Gln Ser Ser Ile Pro Pro	100	105	110	
30	Asn Pro Gly Lys Thr Ala Lys Pro Ile Ser Asn Pro Thr Asn Leu Ser	115	120	125	
	Ser Lys Arg Asp Ala Glu Gly Gly Ile Val Ser Ser Gly Arg Leu Glu	130	135	140	
35	Gly Leu Asn Ala Pro Glu Asn Tyr Ile Arg Ala Tyr Ser Met Leu Lys	145	150	155	160
	Asn Trp Val Asp Ser Ser Leu Glu Ile Tyr Lys Pro Glu Leu Ser Tyr	165	170	175	
40	Ile Met Tyr Pro Ile Phe Ile Tyr Leu Phe Leu Asn Leu Val Ala Lys	180	185	190	
45	Asn Pro Val Tyr Ala Arg Arg Phe Phe Asp Arg Phe Ser Pro Asp Phe	195	200	205	

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	Lys Asp Phe His Gly Ser Glu Ile Asn Arg Leu Phe Ser Val Asn Ser	
	210	215 220
5	Ile Asp His Ile Lys Glu Asn Glu Val Ala Ser Ala Phe Gln Ser His	
	225	230 235 240
	Lys Tyr Arg Ile Thr Met Ser Lys Thr Thr Leu Asn Leu Leu Leu Tyr	
		245 250 255
10	Phe Leu Asn Glu Asn Glu Ser Ile Gly Gly Ser Leu Ile Ile Ser Val	
		260 265 270
	Ile Asn Gln His Leu Asp Pro Asn Ile Val Glu Ser Val Thr Ala Arg	
		275 280 285
15	Glu Lys Leu Ala Asp Gly Ile Lys Val Leu Ser Asp Ser Glu Asn Gly	
		290 295 300
	Asn Gly Lys Gln Asn Leu Glu Met Asn Ser Val Pro Val Lys Leu Gly	
20		305 310 315 320
	Pro Phe Pro Lys Asp Glu Glu Phe Val Lys Glu Ile Glu Thr Glu Leu	
		325 330 335
25	Lys Ile Lys Asp Asp Gln Glu Lys Gln Leu Asn Gln Gln Thr Ala Gly	
		340 345 350
	Asp Asn Tyr Ser Gly Ala Asn Asn Arg Thr Leu Leu Gln Glu Tyr Lys	
		355 360 365
30	Ala Met Asn Asn Glu Lys Phe Lys Asp Asn Thr Gly Asp Asp Asp Lys	
		370 375 380
	Asp Lys Ile Lys Asp Lys Ile Ala Lys Asp Glu Glu Lys Lys Glu Ser	
35		385 390 395 400
	Glu Leu Lys Val Asp Gly Glu Lys Lys Asp Ser Asn Leu Ser Ser Pro	
		405 410 415
40	Ala Arg Asp Ile Leu Pro Leu Pro Pro Lys Thr Ala Leu Asp Leu Lys	
		420 425 430
	Leu Glu Ile Gln Lys Val Lys Glu Ser Arg Asp Ala Ile Lys Leu Asp	
		435 440 445
45	Asn Leu Gln Leu Ala Leu Pro Ser Val Cys Met Tyr Thr Phe Gln Asn	

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	450	455	460
	Thr Asn Lys Asp Met Ser Cys Leu Asp Phe Ser Asp Asp Cys Arg Ile		
	465	470	475 480
5	Ala Ala Ala Gly Phe Gln Asp Ser Tyr Ile Lys Ile Trp Ser Leu Asp		
	485	490	495
	Gly Ser Ser Leu Asn Asn Pro Asn Ile Ala Leu Asn Asn Asn Asp Lys		
10	500	505	510
	Asp Glu Asp Pro Thr Cys Lys Thr Leu Val Gly His Ser Gly Thr Val		
	515	520	525
15	Tyr Ser Thr Ser Phe Ser Pro Asp Asn Lys Tyr Leu Leu Ser Gly Ser		
	530	535	540
	Glu Asp Lys Thr Val Arg Leu Trp Ser Met Asp Thr His Thr Ala Leu		
	545	550	555 560
20	Val Ser Tyr Lys Gly His Asn His Pro Val Trp Asp Val Ser Phe Ser		
	565	570	575
	Pro Leu Gly His Tyr Phe Ala Thr Ala Ser His Asp Gln Thr Ala Arg		
25	580	585	590
	Leu Trp Ser Cys Asp His Ile Tyr Pro Leu Arg Ile Phe Ala Gly His		
	595	600	605
30	Leu Asn Asp Val Asp Cys Val Ser Phe His Pro Asn Gly Cys Tyr Val		
	610	615	620
	Phe Thr Gly Ser Ser Asp Lys Thr Cys Arg Met Trp Asp Val Ser Thr		
	625	630	635 640
35	Gly Asp Ser Val Arg Leu Phe Leu Gly His Thr Ala Pro Val Ile Ser		
	645	650	655
	Ile Ala Val Cys Pro Asp Gly Arg Trp Leu Ser Thr Gly Ser Glu Asp		
40	660	665	670
	Gly Ile Ile Asn Val Trp Asp Ile Gly Thr Gly Lys Arg Leu Lys Gln		
	675	680	685
45	Met Arg Gly His Gly Lys Asn Ala Ile Tyr Ser Leu Ser Tyr Ser Lys		
	690	695	700

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Glu Gly Asn Val Leu Ile Ser Gly Gly Ala Asp His Thr Val Arg Val
 705 710 715 720
 Trp Asp Leu Lys Lys Ala Thr Thr Glu Pro Ser Ala Glu Pro Asp Glu
 5 725 730 735
 Pro Phe Ile Gly Tyr Leu Gly Asp Val Thr Ala Ser Ile Asn Gln Asp
 740 745 750
 10 Ile Lys Glu Tyr Gly Arg Arg Arg Thr Val Ile Pro Thr Ser Asp Leu
 755 760 765
 Val Ala Ser Phe Tyr Thr Lys Lys Thr Pro Val Phe Lys Val Lys Phe
 770 775 780
 15 Ser Arg Ser Asn Leu Ala Leu Ala Gly Gly Ala Phe Arg Pro
 785 790 795

20 (2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 32 amino acids

(B) TYPE: amino acid

25 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

30

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: RACK1 protein rI, Fig. 1C

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

Gly His Asn Gly Trp Val Thr Gln Ile Ala Thr Thr Pro Gln Phe Pro
 40 1 5 10 15
 Asp Met Ile Leu Ser Ala Ser Arg Asp Lys Thr Ile Ile Met Trp Lys
 20 25 30

45

(2) INFORMATION FOR SEQ ID NO:70:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 31 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: unknown

5

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

10

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: RACK1 protein rII, Fig. 1C

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

Gly His Ser His Phe Val Ser Asp Val Val Ile Ser Ser Asp Gly Gln
1 5 10 15

20

Phe Ala Leu Ser Gly Ser Trp Asp Gly Thr Leu Arg Leu Trp Asp
20 25 30

(2) INFORMATION FOR SEQ ID NO:71:

25

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 31 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: unknown

30

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

35

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: RACK1 protein rIII, Fig. 1C

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

Gly His Thr Lys Asp Val Leu Ser Val Ala Phe Ser Ser Asp Asn Arg
1 5 10 15

45

Gln Ile Val Ser Gly Ser Arg Asp Lys Thr Ile Lys Leu Trp Asn

- 180 -

20

25

30

(2) INFORMATION FOR SEQ ID NO:72:

5 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 33 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: unknown

10 (ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

15

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: RACK1 protein rIV, Fig. 1C

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

Ser His Ser Glu Trp Val Ser Cys Val Arg Phe Ser Pro Asn Ser Ser
1 5 10 15

25 Asn Pro Ile Ile Val Ser Cys Gly Trp Asp Lys Leu Val Lys Val Trp
20 25 30

Asn

30

(2) INFORMATION FOR SEQ ID NO:73:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 31 amino acids

35 (B) TYPE: amino acid

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

40 (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

45 (C) INDIVIDUAL ISOLATE: RACK1 protein rV, Fig. 1C

- 181 -

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

Gly His Thr Gly Tyr Leu Asn Thr Val Thr Val Ser Pro Asp Gly Ser
1 5 10 15
Leu Cys Ala Ser Gly Gly Lys Asp Gly Gln Ala Met Leu Trp Asp
20 25 30

(2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 31 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: RACK1 protein rVI, Fig. 1C

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

Leu Asp Gly Gly Asp Ile Ile Asn Ala Leu Cys Phe Ser Pro Asn Arg
1 5 10 15
Tyr Trp Leu Cys Ala Ala Thr Gly Pro Ser Ile Lys Ile Trp Asp
20 25 30

(2) INFORMATION FOR SEQ ID NO:75:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 33 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

- 182 -

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: RACK1 protein rVII, Fig. 1C

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

Ser Lys Ala Glu Pro Pro Gln Cys Thr Ser Leu Ala Trp Ser Ala Asp
1 5 10 15

10 Gly Gln Thr Leu Phe Ala Gly Tyr Thr Asp Asn Leu Val Arg Val Trp
20 25 30

Gln

15

(2) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 32 amino acids
20 (B) TYPE: amino acid
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

25 (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

30 (C) INDIVIDUAL ISOLATE: Human 55 kDa protein rI, Fig. 11

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

35 Gly His Thr Asp Ala Val Leu Asp Leu Ser Trp Asn Lys Leu Ile Arg
1 5 10 15

Asn Val Leu Ala Ser Ala Ser Ala Asp Asn Thr Val Ile Leu Trp Asp
20 25 30

40

(2) INFORMATION FOR SEQ ID NO:77:

(i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 32 amino acids
(B) TYPE: amino acid

- 183 -

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

5 (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

10 (C) INDIVIDUAL ISOLATE: Human 55 kDa protein rII, Fig. 11

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

15 Ala His Asn Asp Glu Ile Ser Gly Leu Asp Leu Ser Ser Gln Ile Lys
1 5 10 15

Gly Cys Leu Val Thr Ala Ser Ala Asp Lys Tyr Val Lys Ile Trp Asp
20 25 30

(2) INFORMATION FOR SEQ ID NO:78:

(i) SEQUENCE CHARACTERISTICS:

25 (A) LENGTH: 37 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

30

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

35 (vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human 55 kDa protein rIII, Fig. 11

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

40

Val His Ser Arg Asp Met Lys Met Gly Val Leu Phe Cys Ser Ser Cys
1 5 10 15

Cys Pro Asp Leu Pro Phe Ile Tyr Ala Phe Gly Gly Gln Lys Glu Gly
45 20 25 30

- 184 -

Leu Arg Val Trp Asp
35

(2) INFORMATION FOR SEQ ID NO:79:

5

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 31 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: unknown

10

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

15

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: AAC-RICH protein rI, Fig. 12

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

Gly	Asn	Lys	Lys	Lys	Ser	Thr	Ser	Val	Ala	Trp	Asn	Ala	Asn	Gly	Thr
1				5					10					15	
Lys	Ile	Ala	Ser	Ser	Gly	Ser	Asp	Gly	Ile	Val	Arg	Val	Trp	Asn	
				20				25					30		

25

(2) INFORMATION FOR SEQ ID NO:80:

30

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 32 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: unknown

35

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

40

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: AAC-RICH protein rII, Fig. 12

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

- 185 -

Gly His Asp Gly Ser Ile Glu Lys Ile Ser Trp Ser Pro Lys Asn Asn
1 5 10 15

Asp Leu Leu Ala Ser Ala Gly Thr Asp Lys Val Ile Lys Ile Trp Asp
5 20 25 30

(2) INFORMATION FOR SEQ ID NO:81:

10 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: unknown

15 (ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

20

(vi) ORIGINAL SOURCE:

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: AAC-RICH protein rIII, Fig. 12

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

Asp His Leu Ala Leu Ile Asp Leu Pro Thr Ile Lys Thr Leu Lys Ile
1 5 10 15

30 Tyr Lys Phe Asn Gly Glu Glu Leu Asn Gln Val Gly Trp Asp
20 25 30

(2) INFORMATION FOR SEQ ID NO:82:

35 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 31 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: unknown

40 (ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

45

(vi) ORIGINAL SOURCE:

(vi) ORIGINAL SOURCE:

- 186 -

(C) INDIVIDUAL ISOLATE: AAC-RICH protein rIV, Fig. 12

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

5 Gly His Thr Ala Ser Ile Tyr Cys Met Glu Phe Asp Pro Thr Gly Lys
1 5 10 15
Tyr Leu Ala Ala Gly Ser Ala Asp Ser Ile Val Ser Leu Trp Asp
10 20 25 30

(2) INFORMATION FOR SEQ ID NO:83:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 34 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

20

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

25

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: BETA TRCP rI, Fig. 13

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

30 Ile His Cys Arg Ser Glu Thr Ser Lys Gly Val Tyr Cys Leu Gln Tyr
1 5 10 15
Asp Asp Gln Lys Ile Val Ser Gly Leu Arg Asp Asn Thr Ile Lys Ile
35 20 25 30
Trp Asp

40 (2) INFORMATION FOR SEQ ID NO:84:

(i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 28 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: unknown

- 187 -

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

5 (iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: BETA TRCP rII, Fig. 13

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

Gly His Thr Gly Ser Val Leu Cys Leu Gln Tyr Asp Glu Arg Val Ile

1 5 10 15

15

Ile Thr Gly Ser Asp Ser Thr Val Arg Val Trp Asp

20 25

(2) INFORMATION FOR SEQ ID NO:85:

20

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: unknown

25

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

30 (iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: BETA TRCP rIII, Fig. 13

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

Ile His His Cys Glu Ala Val Leu His Leu Arg Phe Asn Asn Gly Met

1 5 10 15

40

Met Val Thr Cys Ser Lys Asp Arg Ser Ile Ala Val Trp Asp

20 25 30

(2) INFORMATION FOR SEQ ID NO:86:

45

(i) SEQUENCE CHARACTERISTICS:

- 188 -

- (A) LENGTH: 29 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: unknown

5 (ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

10

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: BETA TRCP rIV, Fig. 13

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

Gly His Arg Ala Ala Val Asn Val Val Asp Phe Asp Asp Lys Tyr Ile
1 5 10 15

20 Val Ser Ala Ser Gly Asp Arg Thr Ile Lys Val Trp Asn
20 25

(2) INFORMATION FOR SEQ ID NO:87:

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: unknown

30 (ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

35

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: BETA TRCP rV, Fig. 13

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

Gly His Lys Arg Gly Ile Ala Cys Leu Gln Tyr Arg Asp Arg Leu Val
1 5 10 15

45 Val Ser Gly Ser Ser Asp Asn Thr Ile Arg Leu Trp Asp
20 25

- 189 -

(2) INFORMATION FOR SEQ ID NO:88:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 29 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

10 (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- 15 (C) INDIVIDUAL ISOLATE: BETA TRCP rVI, Fig. 13

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

20 Gly His Glu Glu Leu Val Arg Cys Ile Arg Phe Asp Asn Lys Arg Ile
1 5 10 15
Val Ser Gly Ala Tyr Asp Gly Lys Ile Lys Val Trp Asp
20 25

25

(2) INFORMATION FOR SEQ ID NO:89:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 29 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

35 (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- 40 (C) INDIVIDUAL ISOLATE: BETA TRCP rVII, Fig. 13

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

45 Glu His Ser Gly Arg Val Phe Arg Leu Gln Phe Asp Glu Phe Gln Ile
1 5 10 15

- 190 -

Val Ser Ser Ser His Asp Asp Thr Ile Leu Ile Trp Asp
20 25

(2) INFORMATION FOR SEQ ID NO:90:

5

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 31 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: unknown

10

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

15

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: beta-prime-cop rI, Fig. 14

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

Ala His Ser Asp Tyr Ile Arg Cys Ile Ala Val His Pro Thr Gln Pro
1 5 10 15

25

Phe Ile Leu Thr Ser Ser Asp Asp Met Leu Ile Lys Leu Trp Asp
20 25 30

(2) INFORMATION FOR SEQ ID NO:91:

30

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 32 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: unknown

35

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

40

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: beta-prime-cop rII, Fig. 14

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

- 191 -

Gly His Thr His Tyr Val Met Gln Ile Val Ile Asn Pro Lys Asp Asn
 1 5 10 15

Asn Gln Phe Ala Ser Ala Ser Leu Asp Arg Thr Ile Lys Val Trp Gln
 5 20 25 30

(2) INFORMATION FOR SEQ ID NO:92:

- 10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 33 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: unknown

15 (ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

20

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: beta-prime-cop rIII, Fig. 14

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

Gly His Glu Lys Gly Val Asn Cys Ile Asp Tyr Tyr Ser Gly Gly Asp
 1 5 10 15

30 Lys Pro Tyr Leu Ile Ser Gly Ala Asp Asp Arg Leu Val Lys Ile Trp
 20 25 30

Asp

35

(2) INFORMATION FOR SEQ ID NO:93:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 31 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: unknown

40

(ii) MOLECULE TYPE: peptide

45 (iii) HYPOTHETICAL: NO

- 192 -

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: beta-prime-cop rIV, Fig. 14

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

10

Gly His Ala Gln Asn Val Ser Cys Ala Ser Phe His Pro Glu Leu Pro
1 5 10 15

Ile Ile Ile Thr Gly Ser Glu Asp Gly Thr Val Arg Ile Trp His
20 25 30

(2) INFORMATION FOR SEQ ID NO:94:

15

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: unknown

20

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

25

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: CDC4 / CDC20 protein rI, Fig. 15

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

35

Gly His Met Thr Ser Val Ile Thr Cys Leu Gln Phe Glu Asp Asn Tyr
1 5 10 15

Val Ile Thr Gly Ala Asp Asp Lys Met Ile Arg Val Tyr Asp
20 25 30

(2) INFORMATION FOR SEQ ID NO:95:

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: unknown

45

(ii) MOLECULE TYPE: peptide

- 193 -

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

5 (vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: CDC4 / CDC20 protein rII, Fig. 15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

10

Gly His Asp Gly Gly Val Trp Ala Leu Lys Tyr Ala His Gly Gly Ile
1 5 10 15

Leu Val Ser Gly Ser Thr Asp Arg Thr Val Arg Val Trp Asp
15 20 25 30

(2) INFORMATION FOR SEQ ID NO:96:

(i) SEQUENCE CHARACTERISTICS:

20

(A) LENGTH: 33 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

25

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

30 (vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: CDC4 / CDC20 protein rIII, Fig. 15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

35

Gly His Asn Ser Thr Val Arg Cys Leu Asp Ile Val Glu Tyr Lys Asn
1 5 10 15

Ile Lys Tyr Ile Val Thr Gly Ser Arg Asp Asn Thr Leu His Val Trp
40 20 25 30

Lys

45 (2) INFORMATION FOR SEQ ID NO:97:

- 194 -

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: unknown

5

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

10

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: CDC4 / CDC20 protein rIV, Fig. 15

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

Gly His Met Ala Ser Val Arg Thr Val Ser Gly His Gly Asn Ile Val
1 5 10 15

20

Val Ser Gly Ser Tyr Asp Asn Thr Leu Ile Val Trp Asp
20 25

(2) INFORMATION FOR SEQ ID NO:98:

25

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 31 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: unknown

30

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

35

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: CDC4 / CDC20 protein rV, Fig. 15

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

Gly His Thr Asp Arg Ile Tyr Ser Thr Ile Tyr Asp His Glu Arg Lys
1 5 10 15

45

Arg Cys Ile Ser Ala Ser Met Asp Thr Thr Ile Arg Ile Trp Asp

- 195 -

20

25

30

(2) INFORMATION FOR SEQ ID NO:99:

5 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: unknown

10 (ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

15

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: CDC4 / CDC20 protein rVI, Fig. 15

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

Gly His Thr Ala Leu Val Gly Leu Leu Arg Leu Ser Asp Lys Phe Leu
1 5 10 15

Val Ser Ala Ala Ala Asp Gly Ser Ile Arg Gly Trp Asp
20 25

(2) INFORMATION FOR SEQ ID NO:100:

30 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 33 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: unknown

35 (ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

40

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: GBLP-CHLAMIDOMONAS HOMOLOG rI, Fig. 16

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

- 196 -

Gly His Thr Asn Trp Val Thr Ala Ile Ala Thr Pro Leu Asp Pro Ser
 1 5 10 15

Ser Asn Thr Leu Leu Ser Ala Ser Arg Asp Lys Ser Val Leu Val Trp
 5 20 25 30

Glu

10 (2) INFORMATION FOR SEQ ID NO:101:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 amino acids
 (B) TYPE: amino acid
 15 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO
 20

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: GBLP -CHLAMIDOMONAS HOMOLOG rII, Fig.
 25 16

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

Gly His Ser His Phe Val Gln Asp Val Val Ile Ser Ser Asp Gly Gln
 30 1 5 10 15

Phe Cys Leu Thr Gly Ser Trp Asp Gly Thr Leu Arg Leu Trp Asp
 35 20 25 30

(2) INFORMATION FOR SEQ ID NO:102:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 amino acids
 40 (B) TYPE: amino acid
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

45 (iii) HYPOTHETICAL: NO

- 197 -

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: GBLP -CHLAMIDOMONAS HOMOLOG rIII, Fig.

5 16

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

Gly	His	Thr	Lys	Asp	Val	Leu	Ser	Val	Ala	Phe	Ser	Val	Asp	Asn	Arg
1				5					10					15	
Gln	Ile	Val	Ser	Gly	Ser	Arg	Asp	Lys	Thr	Ile	Lys	Leu	Trp	Asn	
				20				25					30		

15 (2) INFORMATION FOR SEQ ID NO:103:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 33 amino acids

(B) TYPE: amino acid

20 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

25

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: GBLP -CHLAMIDOMONAS HOMOLOG rIV, Fig.

30 16

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

Gly	His	Thr	Glu	Trp	Val	Ser	Cys	Val	Arg	Phe	Ser	Pro	Met	Thr	Thr
1				5					10					15	
Asn	Pro	Ile	Ile	Val	Ser	Gly	Gly	Trp	Asp	Lys	Met	Val	Lys	Val	Trp
				20				25					30		
40	Asn														

(2) INFORMATION FOR SEQ ID NO:104:

45 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 31 amino acids

- 198 -

(B) TYPE: amino acid
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

5

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

10

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: GBLP -CHLAMIDOMONAS HOMOLOG rV, Fig.

16

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

Gly His His Gly Tyr Val Asn Thr Val Thr Val Ser Pro Asp Gly Ser
1 5 10 15

20

Leu Cys Ala Ser Gly Gly Lys Asp Gly Ile Ala Met Leu Trp Asp
20 25 30

(2) INFORMATION FOR SEQ ID NO:105:

25

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 32 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: unknown

30

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

35

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: GBLP -CHLAMIDOMONAS HOMOLOG rVI, Fig.

16

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

Ile His Cys Leu Cys Phe Ser Pro Asn Arg Tyr Trp Leu Cys Ala Ala
1 5 10 15

45

Thr Gln Ser Ser Ile Lys Ile Trp Asp Leu Glu Ser Lys Ser Ile Val

- 199 -

20

25

30

(2) INFORMATION FOR SEQ ID NO:106:

5

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 33 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: unknown

10

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

15

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: GBLP -CHLAMIDOMONAS HOMOLOG rvII, Fig.

16

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

Lys Lys Ala Gln Val Pro Tyr Cys Val Ser Leu Ala Trp Ser Ala Asp

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Gly Ser Thr Leu Tyr Ser Gly Tyr Thr Asp Gly Gln Ile Arg Val Trp

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30

30

Ala

(2) INFORMATION FOR SEQ ID NO:107:

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 33 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: unknown

40

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

45

(vi) ORIGINAL SOURCE:

- 200 -

(C) INDIVIDUAL ISOLATE: cop-1 protein rI, Fig. 17

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

5 Met Ser Thr Arg Ser Lys Leu Ser Cys Leu Ser Trp Asn Lys His Glu
1 5 10 15
Lys Asn His Ile Ala Ser Ser Asp Tyr Glu Gly Ile Val Thr Val Trp
10 20 25 30
Asp

15 (2) INFORMATION FOR SEQ ID NO:108:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 amino acids

(B) TYPE: amino acid

20 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

25

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: cop-1 protein rII, Fig. 17

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

35 Glu Lys Arg Ala Trp Ser Val Asp Phe Ser Arg Thr Glu Pro Ser Met
1 5 10 15
Leu Val Ser Gly Ser Asp Asp Cys Lys Val Lys Val Trp Cys
20 25 30

40 (2) INFORMATION FOR SEQ ID NO:109:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 amino acids

(B) TYPE: amino acid

45 (D) TOPOLOGY: unknown

- 201 -

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

5 (iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: cop-1 protein rIII, Fig. 17

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

Gly His Lys Lys Ala Val Ser Tyr Met Lys Phe Leu Ser Asn Asn Glu
1 5 10 15

15

Leu Ala Ser Ala Ser Thr Asp Ser Thr Leu Arg Leu Trp Asp
20 25 30

(2) INFORMATION FOR SEQ ID NO:110:

20

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 32 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: unknown

25

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

30 (iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Coronin (p55) rI, Fig. 19

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

Gly His Lys Ser Ala Val Leu Asp Ile Ala Phe His Pro Phe Asn Glu
1 5 10 15

40

Asn Leu Val Gly Ser Val Ser Glu Asp Cys Asn Ile Cys Ile Trp Gly
20 25 30

45 (2) INFORMATION FOR SEQ ID NO:111:

- 202 -

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 32 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: unknown

5

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

10

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Coronin (p55) rII, Fig. 19

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

Gly His Lys Arg Lys Val Gly Thr Ile Ser Phe Gly Pro Val Ala Asp

1 5 10 15

20

Asn Val Ala Val Thr Ser Ser Gly Asp Phe Leu Val Lys Thr Trp Asp

20 25 30

25 (2) INFORMATION FOR SEQ ID NO:112:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 31 amino acids

(B) TYPE: amino acid

30

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

35

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Coronin (p55) rIII, Fig. 19

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

Gly His Ser Asp Met Ile Thr Ser Cys Glu Trp Asn His Asn Gly Ser

45 1 5 10 15

- 203 -

Gln Ile Val Thr Thr Cys Lys Asp Lys Lys Ala Arg Val Phe Asp
20 25 30

(2) INFORMATION FOR SEQ ID NO:113:

5

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 38 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: unknown

10

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

15

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: CORO PROTEIN rI, Fig. 18

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

Arg His Val Phe Ala Ala Gln Pro Lys Lys Glu Glu Cys Tyr Gln Asn
1 5 10 15

25

Leu Lys Thr Lys Ser Ala Val Trp Asp Ser Asn Tyr Val Ala Ala Asn
20 25 30

30

Thr Arg Tyr Ile Trp Asp
35

(2) INFORMATION FOR SEQ ID NO:114:

35

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 32 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: unknown

40

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

45

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: CORO PROTEIN rII, Fig. 18

- 204 -

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

Gly His Lys Ser Ala Val Leu Asp Ile Ala Phe His Pro Phe Asn Glu
 1 5 10 15
 Asn Leu Val Gly Ser Val Ser Glu Asp Cys Asn Ile Cys Ile Trp Gly
 20 25 30

10

(2) INFORMATION FOR SEQ ID NO:115:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 32 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: unknown

15

(ii) MOLECULE TYPE: peptide

20

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: CORO PROTEIN rIII, Fig. 18

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

Gly His Lys Arg Lys Val Gly Thr Ile Ser Phe Gly Pro Val Ala Asp
 1 5 10 15
 Asn Val Ala Val Thr Ser Ser Gly Asp Phe Leu Val Lys Thr Trp Asp
 20 25 30

35

(2) INFORMATION FOR SEQ ID NO:116:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: unknown

40

(ii) MOLECULE TYPE: peptide

45

(iii) HYPOTHETICAL: NO

- 205 -

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: CORO PROTEIN rIV, Fig. 18

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

Gly His Ser Asp Met Ile Thr Ser Cys Glu His Asn Gly Ser Gln Ile
10 1 5 10 15
Val Thr Thr Cys Lys Asp Lys Lys Ala Arg Val Phe Asp
20 25

15 (2) INFORMATION FOR SEQ ID NO:117:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 31 amino acids

(B) TYPE: amino acid

20 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

25

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: CSTF 50kDa rI, Fig. 20

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

Asp His Val Asp Glu Val Thr Cys Leu Ala Phe His Pro Thr Glu Gln
35 1 5 10 15
Ile Leu Ala Ser Gly Ser Arg Asp Tyr Thr Leu Lys Leu Phe Asp
20 25 30

40 (2) INFORMATION FOR SEQ ID NO:118:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 31 amino acids

(B) TYPE: amino acid

45 (D) TOPOLOGY: unknown

- 206 -

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

5 (iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: CSTF 50kDa rII, Fig. 20

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

Asp His Val Asp Glu Val Thr Cys Leu Ala Phe His Pro Thr Glu Gln
1 5 10 15

15

Ile Leu Ala Ser Gly Ser Arg Asp Tyr Thr Leu Lys Leu Phe Asp
20 25 30

20 (2) INFORMATION FOR SEQ ID NO:119:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 32 amino acids

(B) TYPE: amino acid

25 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

30

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: CSTF 50kDa rIII, Fig. 20

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

Ala His Asp Gly Ala Glu Val Cys Ser Ala Ile Phe Ser Lys Asn Ser
1 5 10 15

40

Lys Tyr Ile Leu Ser Ser Gly Lys Asp Ser Val Ala Lys Leu Trp Glu
20 25 30

45

(2) INFORMATION FOR SEQ ID NO:120:

- 207 -

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: unknown

5

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

10

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: CSTF 50kDa rIV, Fig. 20

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

Val His Arg Thr Gln Ala Val Phe Asn His Thr Glu Asp Tyr Val Leu
1 5 10 15

20

Leu Pro Asp Glu Arg Thr Ile Ser Leu Cys Cys Trp Asp
20 25

(2) INFORMATION FOR SEQ ID NO:121:

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: unknown

30

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

35

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: CSTF 50kDa rV, Fig. 20

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

Gly His Asn Asn Ile Val Arg Cys Ile Val His Ser Pro Thr Asn Pro
1 5 10 15

45

Gly Phe Met Thr Cys Ser Asp Asp Phe Arg Ala Arg Phe Trp Tyr

- 208 -

20

25

30

(2) INFORMATION FOR SEQ ID NO:122:

5 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 31 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: unknown

10 (ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

15

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: G- BETA DROSOPH rI, Fig. 23

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

Gly His Leu Ala Lys Ile Tyr Ala Met His Trp Gly Asn Asp Ser Arg
1 5 10 15

25 Asn Leu Val Ser Ala Ser Gln Asp Gly Lys Leu Ile Val Trp Asp
20 25 30

(2) INFORMATION FOR SEQ ID NO:123:

30 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: unknown

35 (ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

40

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: G- BETA DROSOPH rII, Fig. 23

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

- 209 -

Gly His Gly Gly Tyr Leu Ser Cys Cys Arg Phe Leu Asp Asp Asn Gln
 1 5 10 15

Ile Val Thr Ser Ser Gly Asp Met Ser Cys Gly Leu Trp Asp
 5 20 25 30

(2) INFORMATION FOR SEQ ID NO:124:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 31 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

15

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

20 (vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: G- BETA DROSOPH rIII, Fig. 23

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

25

Gly His Thr Gly Asp Val Met Ala Leu Ser Leu Ala Pro Gln Cys Lys
 1 5 10 15

Thr Phe Val Ser Gly Ala Cys Asp Ala Ser Ala Lys Leu Trp Asp
 30 20 25 30

(2) INFORMATION FOR SEQ ID NO:125:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 31 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

40

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

45 (vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: G- BETA DROSOPH rIV, Fig. 23

- 210 -

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

Gly His Glu Ser Asp Ile Asn Ala Val Thr Phe Phe Pro Asn Gly Gln
1 5 10 15
Ala Phe Ala Thr Gly Ser Asp Asp Ala Thr Cys Arg Leu Phe Asp
20 25 30

(2) INFORMATION FOR SEQ ID NO:126:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 34 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: G- BETA DROSOPH rV, Fig. 23

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

Ser His Asp Asn Ile Ile Cys Gly Ile Thr Ser Val Ala Phe Ser Lys
1 5 10 15
Ser Gly Arg Leu Leu Leu Ala Gly Tyr Asp Asp Phe Asn Cys Asn Val
20 25 30
Trp Asp

(2) INFORMATION FOR SEQ ID NO:127:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 31 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

- 211 -

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: G- BETA DROSOPH rVI, Fig. 23

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

Gly His Asp Asn Arg Val Ser Cys Leu Gly Val Thr Glu Asn Gly Met
1 5 10 15
Ala Val Ala Thr Gly Ser Trp Asp Ser Phe Leu Arg Val Trp Asn
20 25 30

15 (2) INFORMATION FOR SEQ ID NO:128:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 32 amino acids

(B) TYPE: amino acid

20 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

25

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: G-BETA HUMAN rI, Fig. 24

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

Gly His Asn Gly Trp Val Thr Gln Ile Ala Thr Thr Pro Gln Phe Pro
1 5 10 15
Asp Met Ile Leu Ser Ala Ser Arg Asp Lys Thr Ile Ile Met Trp Lys
20 25 30

40 (2) INFORMATION FOR SEQ ID NO:129:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 31 amino acids

(B) TYPE: amino acid

45 (D) TOPOLOGY: unknown

- 212 -

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

5 (iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: G-BETA HUMAN rII, Fig. 24

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

Gly His Ser His Phe Val Ser Asp Val Val Ile Ser Ser Asp Gly Gln

1 5 10 15

15

Phe Ala Leu Ser Gly Ser Trp Asp Gly Thr Leu Arg Leu Trp Asp

20 25 30

(2) INFORMATION FOR SEQ ID NO:130:

20

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 31 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: unknown

25

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

30

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: G-BETA HUMAN rIII, Fig. 24

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

Gly His Thr Lys Asp Val Leu Ser Val Ala Phe Ser Ser Asp Asn Arg

1 5 10 15

40

Gln Ile Val Ser Gly Ser Arg Asp Lys Thr Ile Lys Leu Trp Asn

20 25 30

(2) INFORMATION FOR SEQ ID NO:131:

45

(i) SEQUENCE CHARACTERISTICS:

- 213 -

- (A) LENGTH: 33 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: unknown

5 (ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

10

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: G-BETA HUMAN rIV, Fig. 24

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

15

Ser His Ser Glu Trp Val Ser Cys Val Arg Phe Ser Pro Asn Ser Ser
1 5 10 15

Asn Pro Ile Ile Val Ser Cys Gly Trp Asp Lys Leu Val Lys Val Trp
20 25 30

Asn

25 (2) INFORMATION FOR SEQ ID NO:132:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: unknown

30

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

35

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: G-BETA HUMAN rV, Fig. 24

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

Gly His Thr Gly Tyr Leu Asn Thr Val Thr Val Ser Pro Asp Gly Ser
45 1 5 10 15

- 214 -

Leu Cys Ala Ser Gly Gly Lys Asp Gly Gln Ala Met Leu Trp Asp
 20 25 30

(2) INFORMATION FOR SEQ ID NO:133:

5

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 36 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: unknown

10

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

15

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: G-BETA HUMAN rVI, Fig. 24

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:

Lys His Leu Tyr Thr Leu Asp Gly Gly Asp Ile Ile Asn Ala Leu Cys
 1 5 10 15

25

Phe Ser Pro Asn Arg Tyr Trp Leu Cys Ala Ala Thr Gly Pro Ser Ile
 20 25 30

30

Lys Ile Trp Asp
 35

(2) INFORMATION FOR SEQ ID NO:134:

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 31 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: unknown

40

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

45

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: G-BETA HUMAN rVII, Fig. 24

- 215 -

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

Ala Glu Pro Pro Gln Cys Thr Ser Leu Ala Trp Ser Ala Asp Gly Gln
5 1 5 10 15
Thr Leu Phe Ala Gly Tyr Thr Asp Asn Leu Val Arg Val Trp Gln
 20 25 30

10 (2) INFORMATION FOR SEQ ID NO:135:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 31 amino acids

(B) TYPE: amino acid

15 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

20

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: G-Beta 1 bovine rI, Fig. 21

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:

Gly His Leu Ala Lys Ile Tyr Ala Met His Trp Gly Thr Asp Ser Arg
30 1 5 10 15
Leu Leu Val Ser Ala Ser Gln Asp Gly Lys Leu Ile Ile Trp Asp
 20 25 30

35 (2) INFORMATION FOR SEQ ID NO:136:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 amino acids

(B) TYPE: amino acid

40 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

45

(iv) ANTI-SENSE: NO

- 216 -

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: G-Beta 1 bovine rII, Fig. 21

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

Gly His Thr Gly Tyr Leu Ser Cys Cys Arg Phe Leu Asp Asp Asn Gln
1 5 10 15
Ile Val Thr Ser Ser Gly Asp Thr Thr Cys Ala Leu Trp Asp
20 25 30

(2) INFORMATION FOR SEQ ID NO:137:

15 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 31 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: unknown

20 (ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

25

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: G-Beta 1 bovine rIII, Fig. 21

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:

Gly His Thr Gly Asp Val Met Ser Leu Ser Leu Ala Pro Asp Thr Arg
1 5 10 15
Leu Phe Val Ser Gly Ala Cys Asp Ala Ser Ala Lys Leu Trp Asp
20 25 30

(2) INFORMATION FOR SEQ ID NO:138:

40 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 31 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: unknown

45 (ii) MOLECULE TYPE: peptide

- 217 -

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

5 (vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: G-Beta 1 bovine rIV, Fig. 21

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:

10

Gly His Glu Ser Asp Ile Asn Ala Ile Cys Phe Phe Pro Asn Gly Asn
1 5 10 15

Ala Phe Ala Thr Gly Ser Asp Asp Ala Thr Cys Arg Leu Phe Asp
15 20 25 30

(2) INFORMATION FOR SEQ ID NO:139:

(i) SEQUENCE CHARACTERISTICS:

20

(A) LENGTH: 34 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

25

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

30 (vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: G-Beta 1 bovine rV, Fig. 21

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:

35

Ser His Asp Asn Ile Ile Cys Gly Ile Thr Ser Val Ser Phe Ser Lys
1 5 10 15

Ser Gly Arg Leu Leu Leu Ala Gly Tyr Asp Asp Phe Asn Cys Asn Val
40 20 25 30

Trp Asp

45 (2) INFORMATION FOR SEQ ID NO:140:

- 218 -

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 31 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: unknown

5

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

10

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: G-Beta 1 bovine rVI, Fig. 21

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

Gly His Asp Asn Arg Val Ser Cys Leu Gly Val Thr Asp Asp Gly Met
1 5 10 15

20

Ala Val Ala Thr Gly Ser Trp Asp Ser Phe Leu Lys Ile Trp Asn
20 25 30

(2) INFORMATION FOR SEQ ID NO:141:

25

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 31 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: unknown

30

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

35

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: G-Beta-bovine(2) rI, Fig. 22

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:

Gly His Leu Ala Lys Ile Tyr Ala Met His Trp Gly Thr Asp Ser Arg
1 5 10 15

45

Leu Leu Val Ser Ala Ser Gln Asp Gly Lys Leu Ile Ile Trp Asp

- 219 -

20

25

30

(2) INFORMATION FOR SEQ ID NO:142:

5 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: unknown

10 (ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

15

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: G-Beta-bovine(2) rII, Fig. 22

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

Gly His Thr Gly Tyr Leu Ser Cys Cys Arg Phe Leu Asp Asp Asn Gln
1 5 10 15

Ile Ile Thr Ser Ser Gly Asp Thr Thr Cys Ala Leu Trp Asp
20 25 30

(2) INFORMATION FOR SEQ ID NO:143:

30 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 31 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: unknown

35 (ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

40

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: G-Beta-bovine(2) rIII, Fig. 22

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:

- 220 -

Gly His Ser Gly Asp Val Met Ser Leu Ser Leu Ala Pro Asp Gly Arg
 1 5 10 15

Thr Phe Val Ser Gly Ala Cys Asp Ala Ser Ile Lys Leu Trp Asp
 5 20 25 30

(2) INFORMATION FOR SEQ ID NO:144:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 31 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

15

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

20

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: G-Beta-bovine(2) rIV, Fig. 22

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:

25

Gly His Glu Ser Asp Ile Asn Ala Val Ala Phe Phe Pro Asn Gly Tyr
 1 5 10 15

Ala Phe Thr Thr Gly Ser Asp Asp Ala Thr Cys Arg Leu Phe Asp
 30 20 25 30

(2) INFORMATION FOR SEQ ID NO:145:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 34 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

40

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

45

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: G-Beta-bovine(2) rV, Fig. 22

- 221 -

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:145:

Ser His Asp Asn Ile Ile Cys Gly Ile Thr Ser Val Ala Phe Ser Arg
 5 1 5 10 15
 Ser Gly Arg Leu Leu Leu Ala Gly Tyr Asp Asp Phe Asn Cys Asn Ile
 20 25 30
 10 Trp Asp

(2) INFORMATION FOR SEQ ID NO:146:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 31 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: unknown

20 (ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

25

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: G-Beta-bovine(2) rVI, Fig. 22

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:

30

Gly His Asp Asn Arg Val Ser Cys Leu Gly Val Thr Asp Asp Gly Met
 1 5 10 15

35 Ala Val Ala Thr Gly Ser Trp Asp Ser Phe Leu Lys Ile Trp Asn
 20 25 30

(2) INFORMATION FOR SEQ ID NO:147:

40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 31 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

45

(iii) HYPOTHETICAL: NO

- 222 -

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: G-Beta2(Human) rI, Fig. 25

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:147:

10 Gly His Leu Ala Lys Ile Tyr Ala Met His Trp Gly Thr Asp Ser Arg
 1 5 10 15

 Leu Leu Val Ser Ala Ser Gln Asp Gly Lys Leu Ile Ile Trp Asp
 20 25 30

15 (2) INFORMATION FOR SEQ ID NO:148:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 amino acids

(B) TYPE: amino acid

20 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

25

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: G-Beta2(Human) rII, Fig. 25

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:148:

35 Gly His Thr Gly Tyr Leu Ser Cys Cys Arg Phe Leu Asp Asp Asn Gln
 1 5 10 15

 Ile Ile Thr Ser Ser Gly Asp Thr Thr Cys Ala Leu Trp Asp
 20 25 30

40 (2) INFORMATION FOR SEQ ID NO:149:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 31 amino acids

(B) TYPE: amino acid

45 (D) TOPOLOGY: unknown

- 223 -

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

5 (iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: G-Beta2(Human) rIII, Fig. 25

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:149:

Gly His Ser Gly Asp Val Met Ser Leu Ser Leu Ala Pro Asp Gly Arg
1 5 10 15

15

Thr Phe Val Ser Gly Ala Cys Asp Ala Ser Ile Lys Leu Trp Asp
20 25 30

(2) INFORMATION FOR SEQ ID NO:150:

20

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 31 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: unknown

25

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

30 (iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: G-Beta2(Human) rIV, Fig. 25

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:150:

Gly His Glu Ser Asp Ile Asn Ala Val Ala Phe Phe Pro Asn Gly Tyr
1 5 10 15

40

Ala Phe Thr Thr Gly Ser Asp Asp Ala Thr Cys Arg Leu Phe Asp
20 25 30

(2) INFORMATION FOR SEQ ID NO:151:

45

(i) SEQUENCE CHARACTERISTICS:

- 224 -

(A) LENGTH: 34 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: unknown

5 (ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

10

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: G-Beta2(Human) rV, Fig. 25

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:151:

Ser His Asp Asn Ile Ile Cys Gly Ile Thr Ser Val Ala Phe Ser Arg
1 5 10 15

20 Ser Gly Arg Leu Leu Leu Ala Gly Tyr Asp Asp Phe Asn Cys Asn Ile
20 25 30

Trp Asp

25

(2) INFORMATION FOR SEQ ID NO:152:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 31 amino acids

30

(B) TYPE: amino acid

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

35 (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

40

(C) INDIVIDUAL ISOLATE: G-Beta2(Human) rVI, Fig. 25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:152:

45 Gly His Asp Asn Arg Val Ser Cys Leu Gly Val Thr Asp Asp Gly Met
1 5 10 15

- 225 -

Ala Val Ala Thr Gly Ser Trp Asp Ser Phe Leu Lys Ile Trp Asn
 20 25 30

(2) INFORMATION FOR SEQ ID NO:153:

5

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 31 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: unknown

10

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

15

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: G-Beta4(mouse) rI, Fig. 26

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:153:

Gly His Leu Ala Lys Ile Tyr Ala Met His Trp Gly Tyr Asp Ser Arg
 1 5 10 15

25

Leu Leu Val Ser Ala Ser Gln Asp Gly Lys Leu Ile Ile Trp Asp
 20 25 30

(2) INFORMATION FOR SEQ ID NO:154:

30

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: unknown

35

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

40

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: G-Beta4(mouse) rII, Fig. 26

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:154:

- 226 -

Gly His Thr Gly Tyr Leu Ser Cys Cys Arg Phe Leu Asp Asp Gly Gln
1 5 10 15

Ile Ile Thr Ser Ser Gly Asp Thr Thr Cys Ala Leu Trp Asp
5 20 25 30

(2) INFORMATION FOR SEQ ID NO:155:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 31 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

15

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

20

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: G-Beta4(mouse) rIII, Fig. 26

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:155:

25

Gly His Ser Gly Asp Val Met Ser Leu Ser Leu Ser Pro Asp Leu Lys
1 5 10 15

Thr Phe Val Ser Gly Ala Cys Asp Ala Ser Ser Lys Leu Trp Asp
30 20 25 30

(2) INFORMATION FOR SEQ ID NO:156:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 31 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

40

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

45

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: G-Beta4(mouse) rIV, Fig. 26

- 227 -

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:156:

	Gly	His	Ile	Ser	Asp	Ile	Asn	Ala	Val	Ser	Phe	Phe	Pro	Ser	Gly	Tyr
5	1				5					10					15	
	Ala	Phe	Ala	Thr	Gly	Ser	Asp	Asp	Ala	Thr	Cys	Arg	Leu	Phe	Asp	
				20					25					30		

10 (2) INFORMATION FOR SEQ ID NO:157:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 34 amino acids

(B) TYPE: amino acid

15 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

20

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: G-Beta4(mouse) rV, Fig. 26

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:157:

	Ser	His	Asp	Asn	Ile	Ile	Cys	Gly	Ile	Thr	Ser	Val	Ala	Phe	Ser	Lys
30	1				5					10					15	
	Ser	Gly	Arg	Leu	Leu	Leu	Ala	Gly	Tyr	Asp	Asp	Phe	Asn	Cys	Ser	Val
				20					25					30		
35	Trp	Asp														

(2) INFORMATION FOR SEQ ID NO:158:

40 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 31 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: unknown

45 (ii) MOLECULE TYPE: peptide

- 228 -

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

5 (vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: G-Beta4(mouse) rVI, Fig. 26

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:158:

10

Gly His Asp Asn Arg Val Ser Cys Leu Gly Val Thr Asp Asp Gly Met
1 5 10 15

Ala Val Ala Thr Gly Ser Trp Asp Ser Phe Leu Arg Ile Trp Asn
15 20 25 30

(2) INFORMATION FOR SEQ ID NO:159:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 31 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

25

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

30 (vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: GROUCHO PROT. DRSPH rI, Fig. 27

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:159:

35

Thr Ser Ala Ala Pro Ala Cys Tyr Ala Leu Ala Ser Pro Asp Ser Lys
1 5 10 15

Val Cys Phe Ser Cys Cys Ser Asp Gly Asn Ile Ala Val Trp Asp
40 20 25 30

(2) INFORMATION FOR SEQ ID NO:160:

(i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 31 amino acids
(B) TYPE: amino acid

- 229 -

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

5 (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

10 (C) INDIVIDUAL ISOLATE: GROUCHO PROT. DRSPH rII, Fig. 27

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:160:

15 Gly His Thr Asp Gly Ala Ser Cys Ile Asp Ile Ser Pro Asp Gly Ser
1 5 10 15

Arg Leu Trp Thr Gly Gly Leu Asp Asn Thr Val Arg Ser Trp Asp
20 25 30

(2) INFORMATION FOR SEQ ID NO:161:

(i) SEQUENCE CHARACTERISTICS:

25 (A) LENGTH: 31 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

30 (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

35 (C) INDIVIDUAL ISOLATE: GTP binding prt squid rI, Fig. 28

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:161:

40 Gly His Leu Ala Lys Ile Tyr Ala Met His Trp Ala Ser Asp Ser Arg
1 5 10 15

Asn Leu Val Ser Ala Ser Gln Asp Gly Lys Leu Ile Val Trp Asp
20 25 30

45

(2) INFORMATION FOR SEQ ID NO:162:

- 230 -

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: unknown

5

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

10

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: GTP binding prt squid rII, Fig. 28

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:162:

Gly	His	Thr	Gly	Tyr	Leu	Ser	Cys	Cys	Arg	Phe	Ile	Asp	Asp	Asn	Gln
1				5					10					15	
Ile	Val	Thr	Ser	Ser	Gly	Asp	Met	Thr	Cys	Ala	Leu	Trp	Asn		
				20				25					30		

20

(2) INFORMATION FOR SEQ ID NO:163:

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: unknown

30

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

35

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: GTP binding prt squid rIII, Fig. 28

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:163:

Gly	His	Thr	Gly	Asp	Val	Met	Ser	Leu	Ser	Leu	Ala	Pro	Asp	Met	Arg
1				5				10					15		
Thr	Phe	Val	Ser	Gly	Ala	Cys	Asp	Ala	Ser	Ala	Lys	Leu	Phe	Asp	

45

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20

25

30

(2) INFORMATION FOR SEQ ID NO:164:

5 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 31 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: unknown

10 (ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

15

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: GTP binding prt squid rIV, Fig. 28

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:164:

Gly His Glu Ser Asp Ile Asn Ala Ile Thr Tyr Phe Pro Asn Gly Phe
1 5 10 15

Ala Phe Ala Thr Gly Ser Asp Asp Ala Thr Cys Arg Leu Phe Asp
20 25 30

(2) INFORMATION FOR SEQ ID NO:165:

30 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 34 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: unknown

35 (ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

40

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: GTP binding prt squid rV, Fig. 28

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:165:

- 232 -

Ser His Asp Asn Ile Ile Cys Gly Ile Thr Ser Val Ala Phe Ser Lys
 1 5 10 15

Ser Gly Arg Leu Leu Leu Gly Gly Tyr Asp Asp Phe Asn Cys Asn Val :
 5 20 25 30 :

Trp Asp :

10 (2) INFORMATION FOR SEQ ID NO:166:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 amino acids
 (B) TYPE: amino acid
 15 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

20

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: GTP binding prt squid rVI, Fig. 28

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:166:

Gly His Asp Asn Arg Val Ser Cys Leu Gly Val Thr Glu Asp Gly Met
 1 5 10 15

30

Ala Val Ala Thr Gly Ser Trp Asp
 20

(2) INFORMATION FOR SEQ ID NO:167:

35

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 amino acids
 (B) TYPE: amino acid
 40 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

45 (iv) ANTI-SENSE: NO

- 233 -

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: IEF SSP 9306 rI, Fig. 29

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:167:

Gly His Gln Lys Glu Gly Tyr Gly Leu Ser Trp Asn Pro Asn Leu Ser
1 5 10 15

10 Gly His Leu Leu Ser Ala Ser Asp Asp His Thr Ile Cys Leu Trp Asp
20 25 30

(2) INFORMATION FOR SEQ ID NO:168:

15

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 32 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: unknown

20

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

25

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: IEF SSP 9306 rII, Fig. 29

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:168:

Gly His Thr Ala Val Val Glu Asp Val Ser Trp His Leu Leu His Glu
1 5 10 15

35

Ser Leu Phe Gly Ser Val Ala Asp Asp Gln Lys Leu Met Ile Trp Asp
20 25 30

40 (2) INFORMATION FOR SEQ ID NO:169:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 37 amino acids

(B) TYPE: amino acid

45

(D) TOPOLOGY: unknown

- 234 -

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

5 (iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: IEF SSP 9306 rIII, Fig. 29

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:169:

Ser His Ser Val Asp Ala His Thr Ala Glu Val Asn Cys Leu Ser Phe
1 5 10 15

15

Asn Pro Tyr Ser Glu Phe Ile Leu Ala Thr Gly Ser Ala Asp Lys Thr
20 25 30

Val Ala Leu Trp Asp
20 35

(2) INFORMATION FOR SEQ ID NO:170:

(i) SEQUENCE CHARACTERISTICS:

25 (A) LENGTH: 37 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

30

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

35 (vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: IEF SSP 9306 rIV, Fig. 29

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:170:

40

Leu His Ser Phe Glu Ser His Lys Asp Glu Ile Phe Gln Val Gln Trp
1 5 10 15

Ser Pro His Asn Glu Thr Ile Leu Ala Ser Ser Gly Thr Asp Arg Arg
45 20 25 30

- 235 -

Leu Asn Val Trp Asp
35

(2) INFORMATION FOR SEQ ID NO:171:

5

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: unknown

10

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

15

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: IEF SSP 9306 rV, Fig. 29

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:171:

Ile Gly Glu Glu Gln Ser Pro Glu Asp Ala Glu Asp Gly Pro Pro Glu
1 5 10 15

25

Leu Leu Phe Ile His Gly Gly His Thr Ala Lys Ile Ser Asp Phe Ser
20 25 30

Trp Asn

30

(2) INFORMATION FOR SEQ ID NO:172:

(i) SEQUENCE CHARACTERISTICS:

35

- (A) LENGTH: 32 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

40

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

45

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: HUMAN 12.3 rI, Fig. 30

- 236 -

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:172:

5 Gly His Asn Gly Trp Val Thr Gln Ile Ala Thr Thr Pro Gln Phe Pro
 1 5 10 15

 Asp Met Ile Leu Ser Ala Ser Arg Asp Lys Thr Ile Ile Met Trp Lys
 20 25 30

10

(2) INFORMATION FOR SEQ ID NO:173:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 31 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

20 (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

25 (C) INDIVIDUAL ISOLATE: HUMAN 12.3 rII, Fig. 30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:173:

30 Gly His Ser His Phe Val Ser Asp Val Val Ile Ser Ser Asp Gly Gln
 1 5 10 15

 Phe Ala Leu Ser Gly Ser Trp Asp Gly Thr Leu Arg Leu Trp Asp
 20 25 30

35

(2) INFORMATION FOR SEQ ID NO:174:

(i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 31 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

45 (iii) HYPOTHETICAL: NO

- 237 -

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: HUMAN 12.3 rIII, Fig. 30

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:174:

10 Gly His Thr Lys Asp Val Leu Ser Val Ala Phe Ser Ser Asp Asn Arg
1 5 10 15

Gln Ile Val Ser Gly Ser Arg Asp Lys Thr Ile Lys Leu Trp Asn
20 25 30

15 (2) INFORMATION FOR SEQ ID NO:175:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 33 amino acids

(B) TYPE: amino acid

20 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

25

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: HUMAN 12.3 rIV, Fig. 30

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:175:

35 Ser His Ser Glu Trp Val Ser Cys Val Arg Phe Ser Pro Asn Ser Ser
1 5 10 15

Asn Pro Ile Ile Val Ser Cys Gly Trp Asp Lys Leu Val Lys Val Trp
20 25 30

40 Asn

(2) INFORMATION FOR SEQ ID NO:176:

45 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 31 amino acids

- 238 -

(B) TYPE: amino acid
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

5

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

10

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: HUMAN 12.3 rV, Fig. 30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:176:

15

Gly His Thr Gly Tyr Leu Asn Thr Val Thr Val Ser Pro Asp Gly Ser
1 5 10 15

20

Leu Cys Ala Ser Gly Gly Lys Asp Gly Gln Ala Met Leu Trp Asp
20 25 30

(2) INFORMATION FOR SEQ ID NO:177:

(i) SEQUENCE CHARACTERISTICS:

25

(A) LENGTH: 36 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

30

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

35

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: HUMAN 12.3 rVI, Fig. 30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:177:

40

Lys His Leu Tyr Thr Leu Asp Gly Gly Asp Ile Ile Asn Ala Leu Cys
1 5 10 15

45

Phe Ser Pro Asn Arg Tyr Trp Leu Cys Ala Ala Thr Gly Pro Ser Ile
20 25 30

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Lys Ile Trp Asp

35

(2) INFORMATION FOR SEQ ID NO:178:

5

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 38 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: unknown

10

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

15

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: HUMAN 12.3 rVII, Fig. 30

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:178:

Val Ile Ser Thr Ser Ser Lys Ala Glu Pro Pro Gln Cys Thr Ser Leu

1

5

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Ala Trp Ser Ala Asp Gly Gln Thr Leu Phe Ala Gly Tyr Thr Asp Asn

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25

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Leu Val Arg Val Trp Gln

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35

(2) INFORMATION FOR SEQ ID NO:179:

(i) SEQUENCE CHARACTERISTICS:

35

(A) LENGTH: 32 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

40

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

45

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: IEF-7442-human rI, Fig. 31

- 240 -

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:179:

Gly His Gln Lys Glu Gly Tyr Gly Leu Ser Trp Asn Ser Asn Leu Ser
 5 1 5 10 15
 Gly His Leu Leu Ser Ala Ser Asp Asp His Thr Val Cys Leu Trp Asp
 20 25 30

10

(2) INFORMATION FOR SEQ ID NO:180:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: unknown

15

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: IEF-7442-human rII, Fig. 31

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:180:

Gly His Ser Ala Val Val Glu Asp Val Ala Trp His Leu Leu His Glu
 30 1 5 10 15
 Ser Leu Phe Gly Ser Val Ala Asp Asp Gln Lys Leu Met Ile Trp Asp
 20 25 30

35

(2) INFORMATION FOR SEQ ID NO:181:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: unknown

40

(ii) MOLECULE TYPE: peptide

45

(iii) HYPOTHETICAL: NO

- 241 -

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: IEF-7442-human rIII, Fig. 31

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:181:

Ala His Thr Ala Glu Val Asn Cys Leu Ser Phe Asn Pro Tyr Ser Glu
10 1 5 10 15
Phe Ile Leu Ala Thr Gly Ser Ala Asp Lys Thr Val Ala Leu Trp Asp
20 25 30

15

(2) INFORMATION FOR SEQ ID NO:182:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 amino acids
20 (B) TYPE: amino acid
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

25 (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

30 (C) INDIVIDUAL ISOLATE: IEF-7442-human rIV, Fig. 31

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:182:

Val His Trp Ser Pro His Asn Glu Thr Ile Leu Ala Ser Ser Gly Thr
35 1 5 10 15
Asp Arg Arg Leu Asn Val Trp Asp
20

40

(2) INFORMATION FOR SEQ ID NO:183:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 32 amino acids
45 (B) TYPE: amino acid
(D) TOPOLOGY: unknown

- 242 -

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

5 (iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: IEF-7442-human rV, Fig. 31

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:183:

Gly His Thr Ala Lys Ile Ser Asp Phe Ser Trp Asn Pro Asn Glu Pro
1 5 10 15

15

Trp Val Ile Cys Ser Val Ser Glu Asp Asn Ile Met Gln Ile Trp Gln
20 25 30

20 (2) INFORMATION FOR SEQ ID NO:184:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 32 amino acids

(B) TYPE: amino acid

25 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

30

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Insulin-like GF binding
protein complex rI, Fig. 32

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:184:

Ala His Thr Pro Ala Leu Ala Ser Leu Gly Leu Ser Asn Asn Arg Leu
1 5 10 15

Ser Arg Leu Glu Asp Gly Leu Phe Glu Gly Leu Gly Ser Leu Trp Asp
20 25 30

45

- 243 -

(2) INFORMATION FOR SEQ ID NO:185:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 32 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

10 (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- 15 (C) INDIVIDUAL ISOLATE: Insulin-like growth factor bind.
pro. complex-rat rI, Fig. 33

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:185:

20 Thr His Thr Pro Ser Leu Ala Ser Leu Ser Leu Ser Ser Asn Leu Leu
1 5 10 15
Gly Arg Leu Glu Glu Gly Leu Phe Gln Gly Leu Ser His Leu Trp Asp
20 25 30
25

(2) INFORMATION FOR SEQ ID NO:186:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 47 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

35

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

40 (vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Insulin-like growth factor bind.
pro. complex-rat rII, Fig. 33

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:186:

- 244 -

Asn His Leu Glu Thr Leu Ala Glu Gly Leu Phe Ser Ser Leu Gly Arg
1 5 10 15

Val Arg Tyr Leu Ser Leu Arg Asn Asn Ser Leu Gln Thr Phe Ser Pro
5 20 25 30

Gln Pro Gly Leu Glu Arg Leu Trp Leu Asp Ala Asn Pro Trp Asp
35 40 45

10 (2) INFORMATION FOR SEQ ID NO:187:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 amino acids
(B) TYPE: amino acid
15 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO
20

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: LIS1 (human) rI, Fig. 34
25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:187:

Gly His Arg Ser Pro Val Thr Arg Val Ile Phe His Pro Val Phe Ser
30 1 5 10 15

Val Met Val Ser Ala Ser Glu Asp Ala Thr Ile Lys Val Trp Asp
20 25 30

35 (2) INFORMATION FOR SEQ ID NO:188:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 amino acids
(B) TYPE: amino acid
40 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO
45

(iv) ANTI-SENSE: NO

- 245 -

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: LIS1 (human) rII, Fig. 34

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:188:

Gly His Thr Asp Ser Val Gln Asp Ile Ser Phe Asp His Ser Gly Lys
1 5 10 15

10 Leu Leu Ala Ser Cys Ser Ala Asp Met Thr Ile Lys Leu Trp Asp
20 25 30

(2) INFORMATION FOR SEQ ID NO:189:

15 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 31 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: unknown

20 (ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

25

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: LIS1 (human) rIII, Fig. 34

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:189:

Gly His Asp His Asn Val Ser Ser Val Ala Ile Met Pro Asn Gly Asp
1 5 10 15

35 His Ile Val Ser Ala Ser Arg Asp Lys Thr Ile Lys Met Trp Glu
20 25 30

(2) INFORMATION FOR SEQ ID NO:190:

40 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 31 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: unknown

45 (ii) MOLECULE TYPE: peptide

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(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

5 (vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: LIS1 (human) rIV, Fig. 34

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:190:

10

Gly His Arg Glu Trp Val Arg Met Val Arg Pro Asn Gln Asp Gly Thr
1 5 10 15

15

Leu Ile Ala Ser Cys Ser Asn Asp Gln Thr Val Arg Val Trp Val
20 25 30

(2) INFORMATION FOR SEQ ID NO:191:

(i) SEQUENCE CHARACTERISTICS:

20

(A) LENGTH: 26 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

25

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

30

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: LIS1 (human) rV, Fig. 34

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:191:

35

Gly Ser Glu Thr Lys Lys Ser Gly Lys Pro Gly Pro Phe Leu Leu Ser
1 5 10 15

40

Gly Ser Arg Asp Lys Thr Lys Met Trp Asp
20 25

(2) INFORMATION FOR SEQ ID NO:192:

(i) SEQUENCE CHARACTERISTICS:

45

(A) LENGTH: 31 amino acids

(B) TYPE: amino acid

- 247 -

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

5 (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

10 (C) INDIVIDUAL ISOLATE: LIS1 (human) rVI, Fig. 34

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:192:

15 Gly His Asp Asn Trp Val Arg Gly Val Leu Phe His Ser Gly Gly Lys
1 5 10 15

Phe Ile Leu Ser Cys Ala Asp Asp Lys Thr Leu Arg Val Trp Asp
20 25 30

20

(2) INFORMATION FOR SEQ ID NO:193:

(i) SEQUENCE CHARACTERISTICS:

25 (A) LENGTH: 31 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

30 (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

35 (C) INDIVIDUAL ISOLATE: LIS1 (human) rVII, Fig. 34

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:193:

40 Ala His Glu His Phe Val Thr Ser Leu Asp Phe His Lys Thr Ala Pro
1 5 10 15

Tyr Val Val Thr Gly Ser Val Asp Gln Thr Val Lys Val Trp Glu
20 25 30

45

(2) INFORMATION FOR SEQ ID NO:194:

- 248 -

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: unknown

5

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

10

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: MD6 rI, Fig. 35

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:194:

Gly His Ser Ala Arg Val Tyr Ala Leu Tyr Tyr Lys Asp Gly Leu Leu
1 5 10 15

20

Cys Thr Gly Ser Asp Asp Leu Ser Ala Lys Leu Trp Asp
20 25

(2) INFORMATION FOR SEQ ID NO:195:

25

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: unknown

30

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

35

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: MD6 rII, Fig. 35

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:195:

Thr His Thr Cys Ala Ala Val Lys Phe Asp Glu Gln Lys Leu Val Thr
1 5 10 15

45

Gly Ser Phe Asp Asn Thr Val Ala Cys Trp Glu

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20

25

(2) INFORMATION FOR SEQ ID NO:196:

5 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 31 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: unknown

10 (ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

15

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: MD6 rIII, Fig. 35

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:196:

Gly His Thr Gly Ala Val Phe Ser Val Asp Tyr Ser Asp Glu Leu Asp
1 5 10 15

Ile Leu Val Ser Gly Ser Ala Asp Phe Ala Val Lys Val Trp Ala
20 25 30

(2) INFORMATION FOR SEQ ID NO:197:

30 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 40 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: unknown

35 (ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

40

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: MD6 rIV, Fig. 35

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:197:

- 250 -

Gly His Thr Glu Trp Val Thr Lys Val Val Leu Gln Lys Cys Lys Val
 1 5 10 15

Lys Ser Leu Leu His Ser Pro Gly Asp Tyr Ile Leu Leu Ser Ala Asp
 5 20 25 30

Lys Tyr Glu Ile Lys Ile Trp Pro
 35 40

10 (2) INFORMATION FOR SEQ ID NO:198:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 amino acids
 (B) TYPE: amino acid
 15 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

20 (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: MSL1 rI, Fig. 36
 25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:198:

Lys His Asp Gly Gly Val Asn Ser Cys Arg Phe Asn Tyr Lys Asn Ser
 30 1 5 10 15

Leu Ile Leu Ala Ser Ala Asp Ser Asn Gly Arg Leu Asn Leu Trp Asp
 20 25 30

35

(2) INFORMATION FOR SEQ ID NO:199:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 amino acids
 40 (B) TYPE: amino acid
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

45 (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(C) INDIVIDUAL ISOLATE: MSL1 rII, Fig. 36

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:199:

[illegible]

(2) INFORMATION FOR SEQ ID NO:200:

20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 32 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: unknown

25 (ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

30

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: MSL1 rIII, Fig. 36

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:200:

Gly His Met Leu Gly Val Asn Asp Ile Ser Trp Asp Ala His Asp Pro
1 5 10 15

40 Trp Leu Met Cys Ser Val Ala Asn Asp Asn Ser Val His Ile Trp Lys
20 25 30

(2) INFORMATION FOR SEQ ID NO:201:

45

(i) SEQUENCE CHARACTERISTICS:

- 252 -

- (A) LENGTH: 31 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: unknown

5 (ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

10

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: MUS MUSCULUS PROTEIN rI, Fig. 37

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:201:

Gly His Ser Gly Cys Val Asn Thr Val His Phe Asn Gln His Gly Thr
1 5 10 15

20 Leu Leu Ala Ser Gly Ser Asp Asp Leu Lys Val Ile Val Trp Asp
20 25 30

(2) INFORMATION FOR SEQ ID NO:202:

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: unknown

30 (ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

35

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: MUS MUSCULUS PROTEIN rII, Fig. 37

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:202:

Gly His Ile Phe Ile Trp Glu Lys Ser Ser Cys Gln Ile Val Gln Phe
1 5 10 15

45 Leu Glu Ala Asp Glu Gly Gly Thr Ile Asn Cys Ile Asp Ser His Pro
20 25 30

- 253 -

Tyr Leu Pro Val Leu Ala Ser Ser Gly Leu Asp His Glu Val Lys Ile
 35 40 45

5 Trp Ser
 50

(2) INFORMATION FOR SEQ ID NO:203:

10 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: unknown

15 (ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

20 (iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: ORF RB1 rI, Fig. 38

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:203:

Lys His Asp Gly Gly Val Asn Ser Cys Arg Phe Asn Tyr Lys Asn Ser
 1 5 10 15

30 Leu Ile Leu Ala Ser Ala Asp Ser Asn Gly Arg Leu Asn Leu Trp Asp
 20 25 30

(2) INFORMATION FOR SEQ ID NO:204:

35

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: unknown

40

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

45 (iv) ANTI-SENSE: NO

- 254 -

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: ORF RB1 rII, Fig. 38

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:204:

Glu His Gly Thr Ser Val Ser Thr Leu Glu Trp Ser Pro Asn Phe Asp
1 5 10 15

10 Thr Val Leu Ala Thr Ala Gly Gln Glu Asp Gly Leu Val Lys Leu Trp
20 25 30

Asp

15

(2) INFORMATION FOR SEQ ID NO:205:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 32 amino acids
20 (B) TYPE: amino acid
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

25 (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

30 (C) INDIVIDUAL ISOLATE: ORF RB1 rIII, Fig. 38

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:205:

35 Gly His Met Leu Gly Val Asn Asp Ile Ser Trp Asp Ala His Asp Pro
1 5 10 15

Trp Leu Met Cys Ser Val Ala Asn Asp Asn Ser Val His Ile Trp Lys
20 25 30

40

(2) INFORMATION FOR SEQ ID NO:206:

(i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 37 amino acids
(B) TYPE: amino acid

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(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

5 (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

10 (C) INDIVIDUAL ISOLATE: Periodic Trp prt rI, Fig. 39

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:206:

15 Gly His Ile Thr Thr His His Thr Asp Ala Val Leu Ser Met Ala His
1 5 10 15
Asn Lys Tyr Phe Arg Ser Val Leu Ala Ser Thr Ser Ala Asp His Thr
20 25 30
20 Val Lys Leu Trp Asp
35

(2) INFORMATION FOR SEQ ID NO:207:

25

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 47 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: unknown

30

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

35

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Periodic Trp prt rII, Fig. 39

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:207:

45 Ile His Ser Asn Lys Asn Val Ser Ser Ser Glu Trp His Met Leu Asn
1 5 10 15
Gly Ser Ile Leu Leu Thr Gly Gly Tyr Asp Ser Arg Val Ala Leu Thr

- 256 -

20

25

30

Asp Val Arg Ile Ser Asp Glu Ser Gln Met Ser Lys Tyr Trp Ser
35 40 45

5

(2) INFORMATION FOR SEQ ID NO:208:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 30 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

15 (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

20 (C) INDIVIDUAL ISOLATE: PLAP rI, Fig. 40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:208:

25 Gly His Lys Asp Thr Val Cys Ser Leu Ser Ser Gly Lys Phe Gly Thr
1 5 10 15

Leu Leu Ser Gly Ser Trp Asp Thr Thr Ala Lys Val Trp Leu
20 25 30

30

(2) INFORMATION FOR SEQ ID NO:209:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 31 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

40 (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

45 (C) INDIVIDUAL ISOLATE: PLAP rII, Fig. 40

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:209:

Gly His Thr Ala Ala Val Trp Ala Val Lys Ile Leu Pro Glu Gln Gly
 1 5 10 15
 Leu Met Leu Thr Gly Ser Ala Asp Lys Thr Ile Lys Leu Trp Lys
 20 25 30

(2) INFORMATION FOR SEQ ID NO:210:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: PLAP rIII, Fig. 40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:210:

Gly His Glu Asp Cys Val Arg Gly Leu Ala Ile Leu Ser Glu Thr Glu
 1 5 10 15
 Phe Leu Ser Cys Ala Asn Asp Ala Ser Ile Arg Arg Trp Gln
 20 25 30

(2) INFORMATION FOR SEQ ID NO:211:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 31 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

- 258 -

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: PLAP rIV, Fig. 40

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:211:

Gly His Thr Asn Tyr Ile Tyr Ser Ile Ser Val Phe Pro Asn Ser Lys
 1 5 10 15

10 Asp Phe Val Thr Thr Ala Glu Asp Arg Ser Leu Arg Ile Trp Lys
 20 25 30

(2) INFORMATION FOR SEQ ID NO:212:

15 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 32 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: unknown

20 (ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

25

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: RETINOBLASTOMA BINDING PROTEIN -
HUMAN. rI, Fig. 41

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:212:

Gly His Gln Lys Glu Gly Tyr Gly Leu Ser Trp Asn Pro Asn Leu Ser
 1 5 10 15

35

Gly His Leu Leu Ser Ala Ser Asp Asp His Thr Ile Cys Leu Trp Asp
 20 25 30

40 (2) INFORMATION FOR SEQ ID NO:213:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 32 amino acids

(B) TYPE: amino acid

45

(D) TOPOLOGY: unknown

- 259 -

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

5 (iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: RETINOBLASTOMA BINDING PROTEIN -
HUMAN rII, Fig. 41

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:213:

15 Gly His Thr Ala Val Val Glu Asp Val Ser Trp His Leu Leu His Glu
1 5 10 15Ser Leu Phe Gly Ser Val Ala Asp Asp Gln Lys Leu Met Ile Trp Asp
20 25 30

20

(2) INFORMATION FOR SEQ ID NO:214:

(i) SEQUENCE CHARACTERISTICS:

25 (A) LENGTH: 37 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

30 (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

35 (C) INDIVIDUAL ISOLATE: RETINOBLASTOMA BINDING PROTEIN -
HUMAN rIII, Fig. 41

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:214:

40

Ser His Ser Val Asp Ala His Thr Ala Glu Val Asn Cys Leu Ser Phe
1 5 10 1545 Asn Pro Tyr Ser Glu Phe Ile Leu Ala Thr Gly Ser Ala Asp Lys Thr
20 25 30

- 260 -

Val Ala Leu Trp Asp

35

(2) INFORMATION FOR SEQ ID NO:215:

5

(i) SEOUENCE CHARACTERISTICS:

(A) LENGTH: 32 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: unknown

10

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

15

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: RETINOBLASTOMA BINDING PROTEIN -

HUMAN rIV, Fig. 41

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:215:

Ser His Lys Asp Glu Ile Phe Gln Val Gln Trp Ser Pro His Asn Glu

25

1

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10

15

Thr Ile Leu Ala Ser Ser Gly Thr Asp Arg Arg Leu Asn Val Trp Asp

20

25

30

30

(2) INFORMATION FOR SEQ ID NO:216:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 32 amino acids

35

(B) TYPE: amino acid

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

40

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

45

(C) INDIVIDUAL ISOLATE: RETINOBLASTOMA BINDING PROTEIN -

HUMAN rV, Fig. 41

- 261 -

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:216:

Gly His Thr Ala Lys Ile Ser Asp Phe Ser Trp Asn Pro Asn Glu Pro
 5 1 5 10 15
 Trp Val Ile Cys Ser Val Ser Glu Asp Asn Ile Met Gln Val Trp Gln
 20 25 30

10

(2) INFORMATION FOR SEQ ID NO:217:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 amino acids
 15 (B) TYPE: amino acid
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

20 (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

25 (C) INDIVIDUAL ISOLATE: S253 PROTEIN rI, Fig. 42

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:217:

30 Glu His Ala Leu Asp Ile Leu Asp Ala Asn Trp Ser Lys Asn Gly Phe
 1 5 10 15
 Leu Ile Thr Ala Ser Met Asp Lys Thr Ala Lys Leu Trp His
 20 25 30

35

(2) INFORMATION FOR SEQ ID NO:218:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 32 amino acids
 40 (B) TYPE: amino acid
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

45 (iii) HYPOTHETICAL: NO

- 262 -

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: S253 PROTEIN rII, Fig. 42

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:218:

Val His Pro Asp Phe Val Thr Ser Ala Ile Phe Phe Pro Asn Asp Asp
10 1 5 10 15

Arg Phe Ile Ile Thr Gly Cys Leu Asp His Arg Cys Arg Leu Trp Ser
20 25 30

15

(2) INFORMATION FOR SEQ ID NO:219:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 31 amino acids
20 (B) TYPE: amino acid
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

25

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

30 (C) INDIVIDUAL ISOLATE: SOF1 rI, Fig. 43

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:219:

Gly His Arg Asp Gly Val Tyr Ala Ile Ala Lys Asn Tyr Gly Ser Leu
35 1 5 10 15

Asn Lys Leu Ala Thr Gly Ser Ala Asp Gly Val Ile Lys Tyr Trp
20 25 30

40

(2) INFORMATION FOR SEQ ID NO:220:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 35 amino acids
45 (B) TYPE: amino acid
(D) TOPOLOGY: unknown

- 263 -

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

5 (iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: SOF1 rII, Fig. 43

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:220:

Gly Leu Cys Val Thr Gln Pro Arg Phe His Asp Lys Lys Pro Asp Leu
1 5 10 15

15

Lys Ser Gln Asn Phe Met Leu Ser Cys Ser Asp Asp Lys Thr Val Lys
20 25 30

Leu Trp Ser
20 35

(2) INFORMATION FOR SEQ ID NO:221:

(i) SEQUENCE CHARACTERISTICS:

25 (A) LENGTH: 35 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

30

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

35 (vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: SOF1 rIII, Fig. 43

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:221:

40

Gly Leu Ile Arg Thr Phe Asp Gly Glu Ser Ala Phe Gln Gly Ile Asp
1 5 10 15

Ser His Arg Glu Asn Ser Thr Phe Ala Thr Gly Gly Ala Lys Ile His
45 20 25 30

- 264 -

Leu Trp Asp
35

(2) INFORMATION FOR SEQ ID NO:222:

5

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 39 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: unknown

10

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

15

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: SOF1 rIV, Fig. 43

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:222:

Gly His Ser Arg Glu Ile Tyr His Thr Lys Arg Met Gln His Val Phe
1 5 10 15

25

Val Lys Tyr Ser Met Asp Ser Lys Tyr Ile Ile Ser Gly Ser Asp Asp
20 25 30

30

Gly Asn Val Arg Leu Trp Arg
35

(2) INFORMATION FOR SEQ ID NO:223:

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 31 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: unknown

40

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

45

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: STE4-YEAST rI, Fig. 44

- 265 -

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:223:

5 Gly His Asn Asn Lys Ile Ser Asp Phe Arg Trp Ser Arg Asp Ser Lys
 1 5 10 15

 Arg Ile Leu Ser Ala Ser Gln Asp Gly Phe Met Leu Ile Trp Asp
 20 25 30

10 (2) INFORMATION FOR SEQ ID NO:224:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 amino acids

(B) TYPE: amino acid

15 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

20

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: STE4-YEAST rII, Fig. 44

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:224:

30 Gly His Thr Cys Tyr Ile Ser Asp Ile Glu Phe Thr Asp Asn Ala His
 1 5 10 15

 Ile Leu Thr Ala Ser Gly Asp Met Thr Cys Ala Leu Trp Asp
 20 25 30

35 (2) INFORMATION FOR SEQ ID NO:225:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 37 amino acids

(B) TYPE: amino acid

40 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

45

(iv) ANTI-SENSE: NO

- 266 -

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: STE4-YEAST rIII, Fig. 44

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:225:

Asp His Leu Gly Asp Val Leu Ala Leu Ala Ile Pro Glu Glu Pro Asn
1 5 10 15

10 Leu Glu Asn Ser Ser Asn Thr Phe Ala Ser Cys Gly Ser Asp Gly Tyr
20 25 30

Thr Tyr Ile Trp Asp
35

15

(2) INFORMATION FOR SEQ ID NO:226:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 31 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

25 (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

30 (C) INDIVIDUAL ISOLATE: STE4-YEAST rIV, Fig. 44

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:226:

35 Leu Asp Asn Gln Gly Val Val Ser Leu Asp Phe Ser Ala Ser Gly Arg
1 5 10 15

Leu Met Tyr Ser Cys Tyr Thr Asp Ile Gly Cys Val Val Trp Asp
20 25 30

40

(2) INFORMATION FOR SEQ ID NO:227:

(i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 31 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: unknown

- 267 -

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

5 (iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: ST34-YEAST rV, Fig. 44

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:227:

Gly His Gly Gly Arg Val Thr Gly Val Arg Ser Ser Pro Asp Gly Leu
1 5 10 15

15

Ala Val Cys Thr Gly Ser Trp Asp Ser Thr Met Lys Ile Trp Ser
20 25 30

(2) INFORMATION FOR SEQ ID NO:228:

20

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 31 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: unknown

25

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

30 (iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: TRNSCRPTION FCTR TIIIF rI, Fig. 45

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:228:

Gly His Thr Gly Pro Val Tyr Arg Cys Ala Phe Ala Pro Glu Met Asn
1 5 10 15

40

Leu Leu Leu Ser Cys Ser Glu Asp Ser Thr Ile Arg Leu Trp Ser
20 25 30

(2) INFORMATION FOR SEQ ID NO:229:

45

(i) SEQUENCE CHARACTERISTICS:

- 268 -

(A) LENGTH: 31 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: unknown

5 (ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

10

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: TRNSCRPTION FCTR TIIF rII, Fig. 45

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:229:

Gly	His	Val	Tyr	Pro	Val	Trp	Asp	Val	Arg	Phe	Ala	Pro	His	Gly	Tyr
1				5					10					15	

Tyr	Phe	Val	Ser	Cys	Ser	Tyr	Asp	Lys	Thr	Ala	Arg	Leu	Trp	Ala
				20				25					30	

(2) INFORMATION FOR SEQ ID NO:230:

25 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 31 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: unknown

30 (ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

35

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: TRNSCRPTION FCTR TIIF rIII, Fig. 45

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:230:

Gly	His	Leu	Ser	Asp	Val	Asp	Cys	Val	Gln	Phe	His	Pro	Asn	Ser	Asn
1					5				10					15	

Tyr	Val	Ala	Thr	Gly	Ser	Ser	Asp	Arg	Thr	Val	Arg	Leu	Trp	Asp
				20				25					30	

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(2) INFORMATION FOR SEQ ID NO:231:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 31 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

10 (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- 15 (C) INDIVIDUAL ISOLATE: TRANSCRIPTION FACTOR TFIIF rIV, Fig. 45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:231:

20 Gly His Lys Gly Ser Val Ser Ser Leu Ala Phe Ser Ala Cys Gly Arg
1 5 10 15
Tyr Leu Ala Ser Gly Ser Val Asp His Asn Ile Ile Ile Trp Asp
20 25 30

25

(2) INFORMATION FOR SEQ ID NO:232:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 31 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

35 (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- 40 (C) INDIVIDUAL ISOLATE: TRANSCRIPTION FACTOR TFIIF rV, Fig. 45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:232:

45 Arg His Thr Ser Thr Val Thr Thr Ile Thr Phe Ser Arg Asp Gly Thr
1 5 10 15

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Val Leu Ala Ala Ala Gly Leu Asp Asn Asn Leu Thr Leu Trp Asp
20 25 30

(2) INFORMATION FOR SEQ ID NO:233:

5

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 31 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: unknown

10

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

15

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: TUP1 rI, Fig. 46

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:233:

Ser Ser Asp Leu Tyr Ile Arg Ser Val Cys Phe Ser Pro Asp Gly Lys
1 5 10 15

25

Phe Leu Ala Thr Gly Ala Glu Asp Arg Leu Ile Arg Ile Trp Asp
20 25 30

(2) INFORMATION FOR SEQ ID NO:234:

30

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 31 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: unknown

35

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

40

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: TUP1 rII, Fig. 46

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:234:

- 271 -

Gly His Glu Gln Asp Ile Tyr Ser Leu Asp Tyr Phe Pro Ser Gly Asp
1 5 10 15

Lys Leu Val Ser Gly Ser Gly Asp Arg Thr Val Arg Ile Trp Asp
5 20 25 30

(2) INFORMATION FOR SEQ ID NO:235:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 31 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

15

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

20

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: TUP1 rIII, Fig. 46

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:235:

25

Ile Glu Asp Gly Val Thr Thr Val Ala Val Ser Pro Gly Asp Gly Lys
1 5 10 15

Tyr Ile Ala Ala Gly Ser Leu Asp Arg Ala Val Arg Val Trp Asp
30 20 25 30

(2) INFORMATION FOR SEQ ID NO:236:

(i) SEQUENCE CHARACTERISTICS:

35

- (A) LENGTH: 31 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: unknown

40

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

45

(vi) ORIGINAL SOURCE:

- 272 -

(C) INDIVIDUAL ISOLATE: TUP1 rIV, Fig. 46

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:236:

5
Gly His Lys Asp Ser Val Tyr Ser Val Val Phe Thr Arg Asp Gly Gln
1 5 10 15
Ser Val Val Ser Gly Ser Leu Asp Arg Ser Val Lys Leu Trp Asn
10 20 25 30

(2) INFORMATION FOR SEQ ID NO:237:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 31 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

20

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

25

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: TUP1 rV, Fig. 46

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:237:

30
Gly His Lys Asp Phe Val Leu Ser Val Ala Thr Thr Gln Asn Asp Glu
1 5 10 15
Tyr Ile Leu Ser Gly Ser Lys Asp Arg Gly Val Leu Phe Trp Asp
35 20 25 30

(2) INFORMATION FOR SEQ ID NO:238:

(i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 22 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

45

(iii) HYPOTHETICAL: NO

- 273 -

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: TUP1 HOMOLOG rI, Fig. 47

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:238:

Asp Phe Ser Asp Asp Cys Arg Ile Ala Ala Ala Gly Phe Gln Asp Ser
10 1 5 10 15
Tyr Ile Lys Ile Trp Ser
20

15 (2) INFORMATION FOR SEQ ID NO:239:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 31 amino acids

(B) TYPE: amino acid

20 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

25

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: TUP1 HOMOLOG rII, Fig. 47

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:239:

Gly His Ser Gly Thr Val Tyr Ser Thr Ser Phe Ser Pro Asp Asn Lys
35 1 5 10 15
Tyr Leu Leu Ser Gly Ser Glu Asp Lys Thr Val Arg Leu Trp Ser
20 25 30

40 (2) INFORMATION FOR SEQ ID NO:240:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 31 amino acids

(B) TYPE: amino acid

45 (D) TOPOLOGY: unknown

- 274 -

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

5 (iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: TUP1 HOMOLOG rIII, Fig. 47

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:240:

Gly His Asn His Pro Val Trp Asp Val Ser Phe Ser Pro Leu Gly His
1 5 10 15

15

Tyr Phe Ala Thr Ala Ser His Asp Gln Thr Ala Arg Leu Trp Ser
20 25 30

20 (2) INFORMATION FOR SEQ ID NO:241:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 31 amino acids

(B) TYPE: amino acid

25 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

30

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: TUP1 HOMOLOG rIV, Fig. 47

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:241:

Gly His Leu Asn Asp Val Asp Cys Val Ser Phe His Pro Asn Gly Cys
1 5 10 15

40

Tyr Val Phe Thr Gly Ser Ser Asp Lys Thr Cys Arg Met Trp Asp
20 25 30

45 (2) INFORMATION FOR SEQ ID NO:242:

- 275 -

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 31 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: unknown

5

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

10

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: TUP1 HOMOLOG rV, Fig. 47

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:242:

Gly His Thr Ala Pro Val Ile Ser Ile Ala Val Cys Pro Asp Gly Arg

1

5

10

15

20

Trp Leu Ser Thr Gly Ser Glu Asp Gly Ile Ile Asn Val Trp Asp

20

25

30

(2) INFORMATION FOR SEQ ID NO:243:

25

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 32 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: unknown

30

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

35

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: TUP1 HOMOLOG rVI, Fig. 47

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:243:

Gly His Gly Lys Asn Ala Ile Tyr Ser Leu Ser Tyr Ser Lys Glu Gly

1

5

10

15

45

Asn Val Leu Ile Ser Gly Gly Ala Asp His Thr Val Arg Val Trp Asp

- 276 -

20

25

30

(2) INFORMATION FOR SEQ ID NO:244:

5

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 31 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: unknown

10

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

15

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: YCU7 rI, Fig. 48

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:244:

Gly His Phe Asp Ser Thr Asn Ser Leu Ala Tyr Ser Pro Asp Gly Ser
1 5 10 15

25

Arg Val Val Thr Ala Ser Glu Asp Gly Lys Ile Lys Val Trp Asp
20 25 30

(2) INFORMATION FOR SEQ ID NO:245:

30

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 31 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: unknown

35

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

40

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: YCU7 rII, Fig. 48

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:245:

- 277 -

Glu His Thr Ser Ser Val Thr Ala Val Gln Phe Ala Lys Arg Gly Gln
 1 5 10 15

Val Met Phe Ser Ser Ser Leu Asp Gly Thr Val Arg Ala Trp Asp
 5 20 25 30

(2) INFORMATION FOR SEQ ID NO:246:

10 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: unknown

15 (ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

20

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: YCU7 rIII, Fig. 48

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:246:

Arg Ile Gln Phe Asn Cys Leu Ala Val Asp Pro Ser Gly Glu Val Val
 1 5 10 15

Cys Ala Gly Ser Leu Asp Asn Phe Asp Ile His Val Trp Ser
 20 25 30

(2) INFORMATION FOR SEQ ID NO:247:

35 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 31 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: unknown

40 (ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

45

(vi) ORIGINAL SOURCE:

- 278 -

(C) INDIVIDUAL ISOLATE: YCU7 rIV, Fig. 48

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:247:

5
Gly His Glu Gly Pro Val Ser Cys Leu Ser Phe Ser Gln Glu Asn Ser
1 5 10 15
Val Leu Ala Ser Ala Ser Trp Asp Lys Thr Ile Arg Ile Trp Ser
10 20 25 30

(2) INFORMATION FOR SEQ ID NO:248:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 32 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

20

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

25

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: YCW2 PROTEIN rI, Fig. 49

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:248:

30

Gly His Gly Ser Thr Ile Leu Cys Ser Ala Phe Ala Pro His Thr Ser
1 5 10 15
Ser Arg Met Val Thr Gly Ala Gly Asp Asn Thr Ala Arg Ile Trp Asp
35 20 25 30

(2) INFORMATION FOR SEQ ID NO:249:

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 31 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: unknown

45

(ii) MOLECULE TYPE: peptide

- 279 -

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

5 (vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: YCW2 PROTEIN rII, Fig. 49

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:249:

10

Gly His Tyr Asn Trp Val Leu Cys Val Ser Trp Ser Pro Asp Gly Glu
1 5 10 15

Val Ile Ala Thr Gly Ser Met Asp Asn Thr Ile Arg Leu Trp Asp
15 20 25 30

(2) INFORMATION FOR SEQ ID NO:250:

(i) SEQUENCE CHARACTERISTICS:

20

(A) LENGTH: 38 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

25

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

30

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: YCW2 PROTEIN rIII, Fig. 49

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:250:

35

Gly His Ser Lys Trp Ile Thr Ser Leu Ser Trp Glu Pro Ile His Leu
1 5 10 15

Val Lys Pro Gly Ser Lys Pro Arg Leu Ala Ser Ser Ser Lys Asp Gly
20 25 30

40

Thr Ile Lys Ile Trp Asp
35

(2) INFORMATION FOR SEQ ID NO:251:

45

(i) SEQUENCE CHARACTERISTICS:

- 280 -

(A) LENGTH: 30 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: unknown

5 (ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

10

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: YCW2 PROTEIN rIV, Fig. 49

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:251:

Gly His Thr Asn Ser Val Ser Cys Val Lys Trp Gly Gly Gln Gly Leu
1 5 10 15

20 Leu Tyr Ser Gly Ser His Asp Arg Thr Val Arg Val Trp Asp
20 25 30

(2) INFORMATION FOR SEQ ID NO:252:

25 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: unknown

30 (ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

35

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: YCW2 PROTEIN rV, Fig. 49

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:252:

Lys Ile Cys Lys Lys Asn Gly Asn Ser Glu Glu Met Met Val Thr Ala
1 5 10 15

45 Ser Asp Asp Tyr Thr Met Phe Leu Trp Asn
20 25

- 281 -

(2) INFORMATION FOR SEQ ID NO:253:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 25 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

10 (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- 15 (C) INDIVIDUAL ISOLATE: YCW2 PROTEIN rVI, Fig. 49

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:253:

20 Asn His Val Ala Phe Ser Pro Asp Gly Arg Tyr Ile Val Ser Ala Ser
1 5 10 15
Phe Asp Asn Ser Ile Lys Leu Trp Asp
20 25

25

(2) INFORMATION FOR SEQ ID NO:254:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 31 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

35 (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- 40 (C) INDIVIDUAL ISOLATE: YCW2 PROTEIN rVII, Fig. 49

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:254:

45 Gly His Ile Ala Ser Val Tyr Gln Val Ala Trp Ser Ser Asp Cys Arg
1 5 10 15

- 282 -

Leu Leu Val Ser Cys Ser Lys Asp Thr Thr Leu Lys Val Trp Asp
 20 25 30

(2) INFORMATION FOR SEQ ID NO:255:

5

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 35 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: unknown

10

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

15

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: YCW2 PROTEIN rVIII, Fig. 49

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:255:

Ser Val Asp Leu Pro Gly Ile Lys Thr Lys Leu Tyr Val Asp Trp Ser
 1 5 10 15

25

Val Asp Gly Lys Arg Val Cys Ser Gly Gly Lys Asp Lys Met Val Arg
 20 25 30

Leu Trp Thr

35

- 283 -

(2) INFORMATION FOR SEQ ID NO:256:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 29 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

10 (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- 15 (C) INDIVIDUAL ISOLATE: YKL525 rI, Fig. 50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:256:

20 Leu His Leu Tyr Ala Pro Val Phe Tyr Ser Asp Val Phe Arg Val Phe
1 5 10 15
Met Glu His Ala Leu Asp Ile Leu Asp Ala Asn Trp Ser
20 25
25

- 284 -

(2) INFORMATION FOR SEQ ID NO:257:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 32 amino acids

5 (B) TYPE: amino acid

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

10 (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

15 (C) INDIVIDUAL ISOLATE: YKL525 rII, Fig. 50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:257:

20 Val His Pro Asp Phe Val Thr Ser Ala Ile Phe Phe Pro Asn Asp Asp
1 5 10 15

Arg Phe Ile Ile Thr Gly Cys Leu Asp His Arg Cys Arg Leu Trp Ser
20 25 30

25

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(2) INFORMATION FOR SEQ ID NO:258:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 31 amino acids

5 (B) TYPE: amino acid

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

10 (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

15 (C) INDIVIDUAL ISOLATE: yrb 1410 yeast rI, Fig. 51

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:258:

20 Gly His Asn His Pro Val Trp Asp Val Ser Phe Ser Pro Leu Gly His
1 5 10 15

Tyr Phe Ala Thr Ala Ser His Asp Gln Thr Ala Arg Leu Trp Ser
20 25 30

25

- 286 -

(2) INFORMATION FOR SEQ ID NO:259:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 31 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

10 (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- 15 (C) INDIVIDUAL ISOLATE: yrb 1410 yeast rII, Fig. 51

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:259:

20 Gly His Leu Asn Asp Val Asp Cys Val Ser Phe His Pro Asn Gly Cys
1 5 10 15
Tyr Val Phe Thr Gly Ser Ser Asp Lys Thr Cys Arg Met Trp Asp
20 25 30
25

- 287 -

(2) INFORMATION FOR SEQ ID NO:260:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 31 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

10 (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- 15 (C) INDIVIDUAL ISOLATE: yrb 1410 yeast rIII, Fig. 51

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:260:

20 Gly His Thr Ala Pro Val Ile Ser Ile Ala Val Cys Pro Asp Gly Arg
1 5 10 15
Trp Leu Ser Thr Gly Ser Glu Asp Gly Ile Ile Asn Val Trp Asp
20 25 30
25

- 288 -

(2) INFORMATION FOR SEQ ID NO:261:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 32 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

10 (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- 15 (C) INDIVIDUAL ISOLATE: yrb 1410 yeast rIV, Fig. 51

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:261:

20 Gly His Gly Lys Asn Ala Ile Tyr Ser Leu Ser Tyr Ser Lys Glu Gly
1 5 10 15
Asn Val Leu Ile Ser Gly Gly Ala Asp His Thr Val Arg Val Trp Asp
20 25 30
25

- 289 -

(2) INFORMATION FOR SEQ ID NO:262:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 34 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

10 (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- 15 (C) INDIVIDUAL ISOLATE: WD40 Consensus Sequence

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:262:

20 Gly His Ser Ala Ala Leu Ala Ala Leu Ala Leu Ser Pro Asp Ala Ala
1 5 10 15
Ala Ala Ala Leu Ala Ser Gly Ala Arg Asp Ala Thr Leu Arg Leu Trp
20 25 30
25 Asp Leu

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(2) INFORMATION FOR SEQ ID NO:263:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 5 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

10

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

15

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: WRTAA peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:263:

20

Trp Arg Thr Ala Ala

1 5

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(2) INFORMATION FOR SEQ ID NO:264:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 5 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

10

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

15

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: WRTAV peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:264:

20

Trp Arg Thr Ala Val
1 5

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(2) INFORMATION FOR SEQ ID NO:265:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 4 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

10

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

15

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: WRTA peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:265:

20

Trp Arg Thr Ala
1

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Claims

1. A polypeptide composition effective to alter the activity of a first protein, wherein the first protein interacts with a second protein, and the second protein contains at least one WD-40 region,

said polypeptide having between 4 and 50 amino acids whose sequence is the same as a sequence of the same length in the WD-40 region of the second protein.

10

2. The composition of claim 1, wherein said polypeptide inhibits interactions between the first protein and the second protein; and/or wherein said polypeptide is an agonist of the activity of the first protein; and/or wherein said polypeptide is an antagonist of the activity of the first protein.

15

3. The composition of claim 1 or 2, wherein said WD-40 region has an amino acid sequence derived from the group consisting of SEQ ID NO:76-261.

20

4. The composition of claim 3, wherein said WD-40 region has an amino acid sequence selected from the group consisting of SEQ ID NO:76-261.

25

5. The polypeptide composition of claim 1 wherein said polypeptide is coupled to a solid support.

6. A method to bind selectively said first protein which method comprises contacting a sample putatively containing said first protein with the polypeptide composition of claim 5; and removing any unbound components of the sample from said composition.

30

7. A method to assess the interaction of a first protein with a polypeptide having a sequence the same as a sequence of the same length contained in a WD-40 region of a second protein, which method comprises

35

contacting a sample containing said first protein with a polypeptide composition wherein the polypeptide has between 4 and 50 amino acids whose sequence is the same as the sequence of the same length in the WD-40 region of the second protein, and observing any interaction of the first protein with said polypeptide composition.

40

8. A method to assess the ability of a candidate compound to bind a first protein which method comprises contacting said first protein with a polypeptide composition which binds said first protein,

45

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wherein the polypeptide of said composition has between 4 and 50 amino acids whose sequence is the same as a sequence of the same length in a WD-40 region of a second protein which interacts with said first protein, in the presence and absence of said candidate compound; and

5 measuring the binding of said polypeptide in the presence and in the absence of said candidate,

 wherein decreased binding of the polypeptide in the presence as opposed to the absence of said candidate indicates that said candidate binds to said first protein.

10

9. A method to alter the activity of a first protein that interacts with a second protein, where the second protein contains at least one WD-40 region, said method comprising

 selecting a polypeptide having between 4 and 50 amino acids
15 whose sequence is the same as a sequence of the same length in the WD-40 region in the second protein, and

 contacting said polypeptide with said first protein under conditions which allow the formation of a complex between the polypeptide and the first protein, where said interaction is effective to alter the
20 activity of the first protein.

10. The method of claim 9, wherein said contacting is effective to inhibit the interaction between said first and second proteins; and/or wherein said contacting is effective to stimulate the
25 activity of said first protein; and/or wherein said contacting is effective to inhibit the activity of said first protein.

11. The method of any of claims 5-10, wherein said polypeptide is derived from the group consisting of SEQ ID NO:76-261.

30

12. The method of claim 11, wherein said polypeptide is selected from the group consisting of SEQ ID NO:76-261.

13. A composition of DNA molecules which consists of DNA
35 molecules having a nucleotide sequence encoding the polypeptide of any of claims 1-4.

14. A DNA molecule which comprises an expression system for the production of the polypeptide of any of claims 1-4 which expression
40 system comprises a nucleotide sequence encoding said polypeptide operably linked to control sequences capable of effecting the expression of said encoding nucleotide sequence.

15. Recombinant host cells modified to contain the
45 expression system of claim 14.

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16. A method to produce a polypeptide having between 4 and 50 amino acids whose sequence is the same as the sequence of the same length in a WD-40 region of a second protein which interacts with a first protein, which method comprises culturing the cells of claim 15 under conditions wherein said nucleotide sequence is expressed to produce said polypeptide; and

optionally recovering said polypeptide from the culture.

17. A polypeptide composition effective to alter the activity of a protein kinase C, where the protein kinase C interacts with a second protein, and the second protein contains at least one WD-40 region,

said polypeptide having between 4 and 50 amino whose sequence is the same as a sequence of the same length in the WD-40 region of the second protein.

18. The composition of claim 17, wherein said second protein is a receptor for activated protein kinase C.

19. The composition of claim 18, where said second protein has the sequence represented by SEQ ID NO:27.

20. The composition of claim 17, wherein said polypeptide is an agonist of the activity of protein kinase C; and/or wherein said polypeptide is an antagonist of the activity of protein kinase C; and/or wherein said polypeptide inhibits interactions between protein kinase C and the second protein.

21. The composition of claim 20 wherein said polypeptide has the sequence represented by SEQ ID NO:7, SEQ ID NO:4 or SEQ ID NO:2.

22. The composition of claim 17, wherein said WD-40 region has an amino acid sequence derived from the group consisting of SEQ ID NO:69-75.

23. The composition of claim 22, wherein said WD-40 region has an amino acid sequence selected from the group consisting of SEQ ID NO:69-75.

24. The polypeptide composition of claim 17 wherein said polypeptide is coupled to a solid support.

25. A method to bind selectively protein kinase C which method comprises contacting a sample putatively containing protein kinase C with the polypeptide composition of claim 24; and

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removing any unbound components of the sample from said composition.

26. A method to assess the interaction of protein kinase C with a polypeptide having a sequence the same as a sequence of the same length contained in the WD-40 region of a second protein, which method comprises

contacting a sample containing said protein kinase C with a polypeptide composition wherein the polypeptide has between 4 and 50 amino acids whose sequence is the same as the sequence of the same length in the WD-40 region of the second protein, and observing any interaction of the protein kinase C with said polypeptide composition.

27. A method to assess the ability of a candidate compound to bind protein kinase C which method comprises contacting said protein kinase C with a polypeptide composition which binds said protein kinase C, wherein the polypeptide of said composition has between 4 and 50 amino acids whose sequence is the same as a sequence of the same length in a WD-40 region of a second protein which interacts with said protein kinase C, in the presence and absence of said candidate compound; and

measuring the binding of said polypeptide in the presence and in the absence of said candidate,

wherein decreased binding of the polypeptide in the presence as opposed to the absence of said candidate indicates that said candidate binds to said protein kinase C.

28. A method to alter the activity of protein kinase C that interacts with a second protein, where the second protein contains at least one WD-40 region, comprising

selecting a polypeptide having between 4 and 50 amino acids whose sequence is the same as a sequence of the same length in the WD-40 region in the second protein, and

contacting said polypeptide with said protein kinase C under conditions which allow the formation of a complex between the polypeptide and the protein kinase C, where said interaction alters the activity of said protein kinase C.

29. The method of claim 28, wherein said contacting is effective to inhibit the interaction between said protein kinase C and said second protein; and/or wherein said contacting is effective to stimulate the activity of said protein kinase C; and/or wherein said contacting is effective to inhibit the activity of said protein kinase C.

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30. The method of claim 29, wherein said polypeptide has an amino acid sequence represented by SEQ ID NO:2, SEQ ID NO:4 or SEQ ID NO:7.

5 31. The method of claim 28, wherein said polypeptide is derived from the group consisting of SEQ ID NO:69-75.

32. The method of claim 31, wherein said polypeptide is selected from the group consisting of SEQ ID NO:69-75.
10

33. A composition of DNA molecules which consists of DNA molecules having a nucleotide sequence of encoding the polypeptide of any of claims 17-23.

15 34. A DNA molecule which comprises an expression system for the production of the polypeptide of any of claims 17-23 which expression system comprises a nucleotide sequence encoding said polypeptide operably linked to control sequences capable of effecting the expression of said encoding nucleotide sequence.

20 35. Recombinant host cells modified to contain the expression system of claim 34.

25 36. A method to produce a polypeptide having between 4 and 50 amino acids whose sequence is the same as the sequence of the same length in a WD-40 region of a second protein which interacts with protein kinase C, which method comprises culturing the cells of claim 35 under conditions wherein said nucleotide sequence is expressed to produce said polypeptide; and

30 optionally recovering said polypeptide from the culture.

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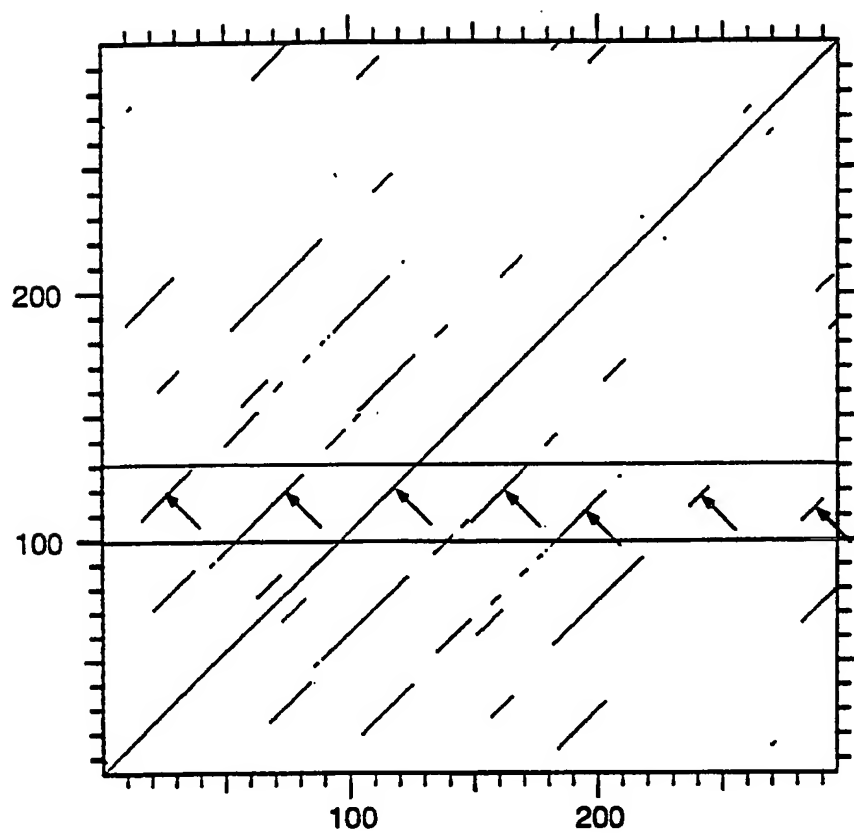
```

1  GGCACGAGGG  GTGCGGTGG  CAGCCGTGG  GTGCTTGGCT  CCCTAAGCTA  TCCGGTGCCA  60
61  TCCTTGTCG  TGCGGGGACT  CGCAACATCT  GCAGCCTTGA  CCGAGCAAAT  GACCCCTCGT
121  GGGACCCCTCA  AGGGCCATAA  TGGATGGGTT  ACACAGATCG  CCACCACTCC  GCAGTTCCCG
181  GACATGATCC  TGTGGCGTC  TCGAGACAAG  ACCATCATCA  TGTGGAAGCT  GACCAGGGAT
241  GAGACCAACT  ACGGCATACC  ACAAGTGCT  CTTGAGGTC  ACTCCCACTT  TGTTAGCGAT
301  GTTGTCATCT  CCTCGATGG  CCAGTTTGCC  CTCTCAGGCT  CCTGGGATGG  AACCTACGC
361  CTCTGGGATC  TCACAACGGG  CACTACCACG  AGAGATTGG  TCGGCCACAC  CAAGGATGTG
421  CTGAGCGTGG  CTTTCTCCTC  TGACAACCGG  CAGATTGTCT  CTGGGTCCCG  AGACAAGACC
481  ATTAAGTTAT  GGAATACTCT  GGGTGTCG  AAGTACACTG  TCCAGGATGA  GAGTCATTCA
541  GAATGGGTGT  CTTGTGTCCG  CTTCTCCCG  AACAGCAGCA  ACCCTATCA?  CGTCTCCTGC
601  GGATGGGACA  AGCTGGTCAA  GGTGTGGAAT  CTGGCTAACT  GCAAGCTAAA  GACCAACCAC
661  ATTGGCCACA  CTGGCTATCT  GAACACAGTG  ACTGTCTCTC  CAGATGGATC  CCTCTGTGCT
721  TCTGGAGGCA  AGGATGGCCA  GGCTATGCTG  TGGGATCTCA  ATGAAGGCAA  GCACCTTTAC
781  ACATTAGATG  GTGGAGACAT  CATCAATGCC  TTGTGCTTCA  GCCCAACCG  CTACTGGCTC
841  TGTGCTGCCA  CTGGCCCCAG  TATCAAGATC  TGGGACTTGG  AGGGCAAGAT  CATGGTAGAT
901  GAACTGAAGC  AAGAAGTTAT  CAGCACCAGC  AGCAAGGCAG  AGCCACCCCA  GTGTACCTCT
961  TTGGCTTGGT  CTGCTGATGG  CCAGACTCTG  TTTGCTGGCT  ATACCGACAA  CTTGGTGCGT
1021  GTATGGCAGG  TGAATATTGG  TACCCGCTAA  AAGTTTATGA  CAGACTCTTA  GAAATAAACT
1081  GGCCTTCTGA  AAAAAAAAAA  AAAAAAAAAA  AAAAA

```

Fig. 1A

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**Fig. 1B**

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Rat	RACK1	MTEQMTLRGTLKGHNGWVTO	IATTPQFPDMILSASRDKTIIMWKLTRDETN(51)	Repeat I
		YGIPQRALRGHSHEVS	DVVISSDGQFALSGSWDGTLRRLWDLT(93)	Repeat II
		TGTTTRRFVGHTKDVL	SVAES8DNQRQIVSGSRDKTIKLNWTLG(136)	Repeat III
		VCKYTVQDESHSEWVSCVRFSPN8SNPIIVSCGWDKLVKVNLA(180)		Repeat IV
		NCKLKTNHIGHTGYLN	TVTVP8DGSGLCASGGKDGQAMLWDL(221)	Repeat V
		NEGKHLTYTLDGGDII	NALCE8PNRYWLCAATGP8IKIWDLEGGKIIIVDE(269)	Repeat VI
		LKQEVISTSSKAEPPEOCTSLAWSADGQTLFAGYTDNLVVRVQVTIGTR(317)		Repeat VII

Consensus sequence of repeats:

Rat RACK1	GHS--V-----V---SSD---ILSG--D-TIKLW-L
Human Gp2	GH---I---SVA---DG---LVTGS-D--C-IWDL

Fig. 1C

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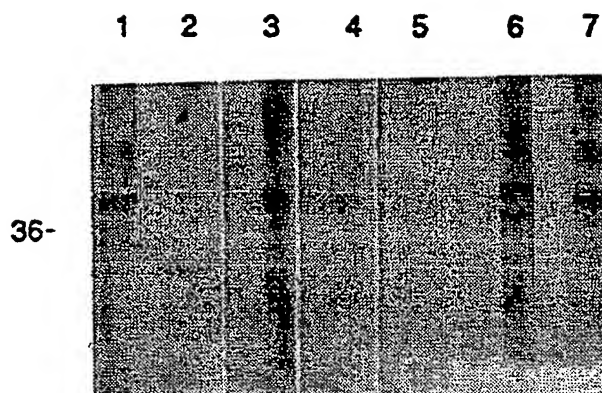


Fig. 2

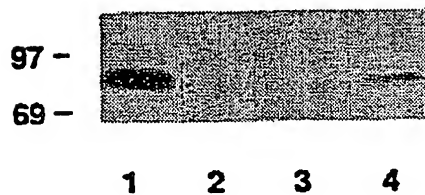


Fig. 3

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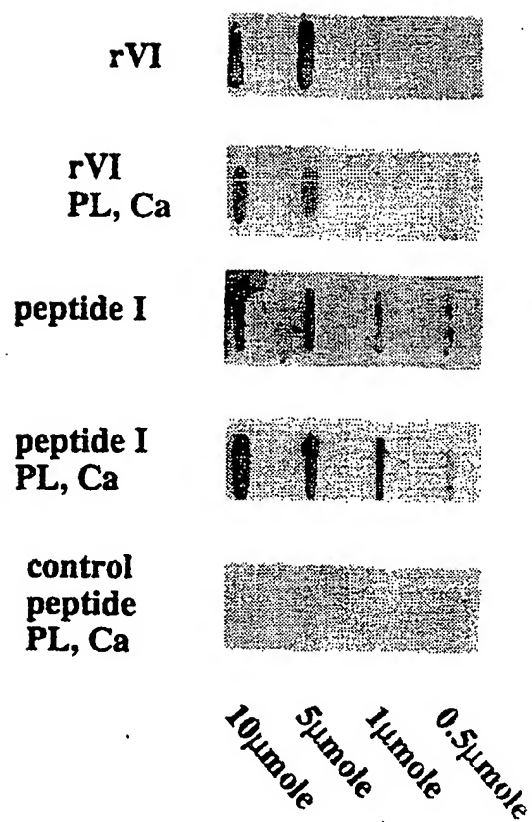


Fig. 4

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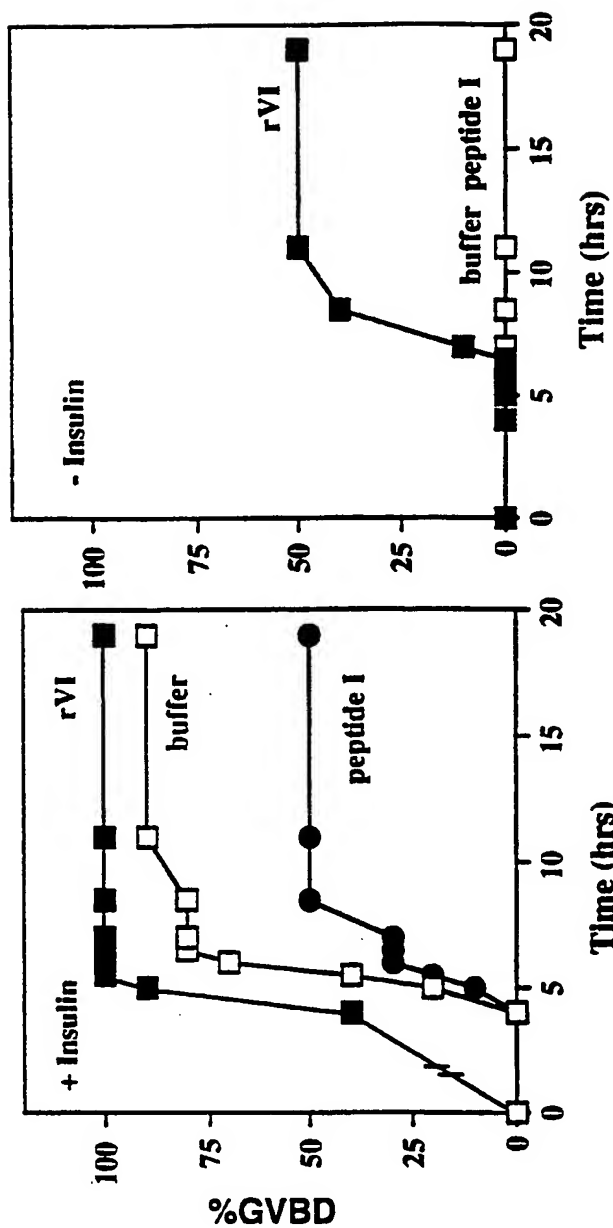


Fig. 5B

Fig. 5A

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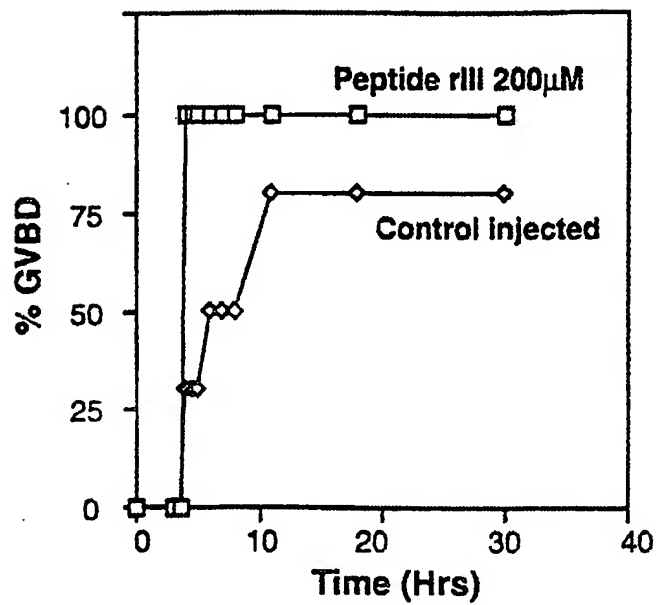


Fig. 5C

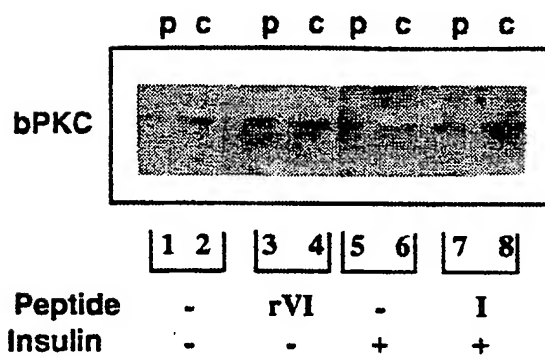


Fig. 6

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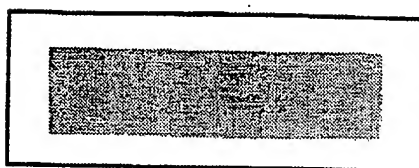
80- 78-									
	1	2	3	4	5	6	7	8	9
Arg-c	-	+	+	+	+	+	+	+	+
PS(mg)	-	50	50	2.5	2.5	2.5	2.5	2.5	2.5
DG (0.8 µg)	-	+	-	-	-	-	-	-	-
Ca (mM)	-	1000	1000	50	50	50	50	50	50
Peptide (10mM)	-	-	-	-	rVI	rVI	rVI	C	I
Time of Incubation (min)	30	30	30	30	5	15	30	30	30

Fig. 7



	1	2	3	4	5	6
PS/DG/Ca	+	-	-	-	-	-
EGTA	-	+	-	-	-	-
Anti-pseudo- substrate antibodies	-	-	+	-	-	-
peptides (10mM)	-	-	-	rVI	I	C

Fig. 8

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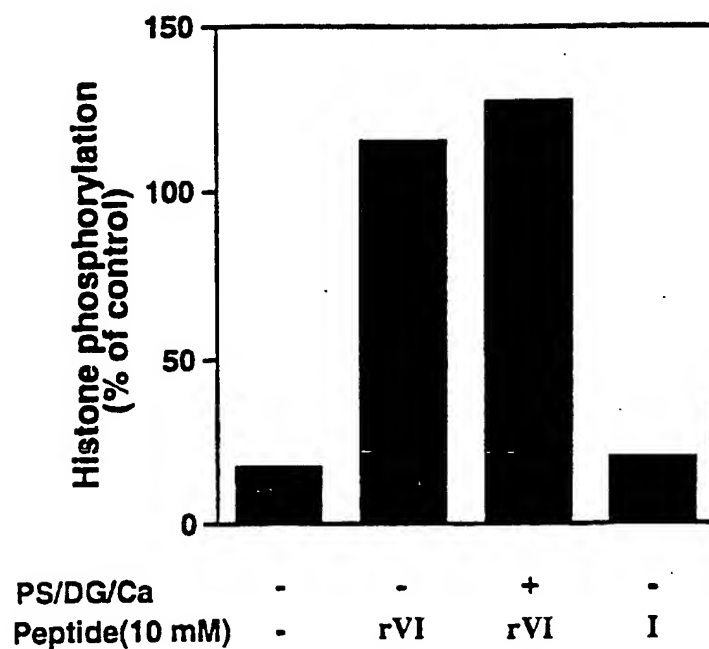


Fig. 9

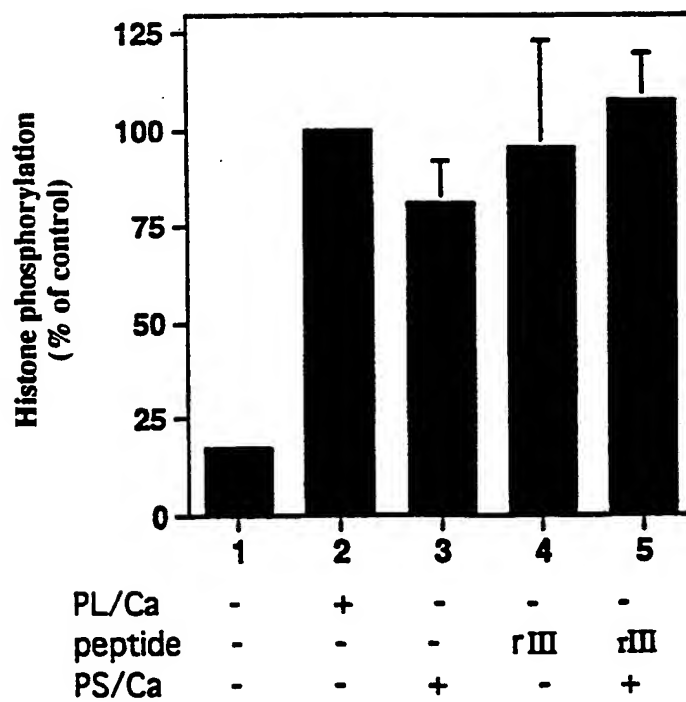


Fig. 10

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Fig. 11

Human 56 kDa protein (PWP homolog)

1 mnrsrqvtcv awvrcgvake tpdkvelske evkrliaeak eklqeeggs
51 deeetgspse dgmqsartqa rprepledgd peddrtlddd elaeydlky
101 deegdpdaet lgesllglvt ygsndqpyv tlkdteqyer edflikpsdn
151 livcgraeqd qcnlevhvyn qeedsfyvhh dillsaypls vewlnfdpsp
201 ddstgnyia vgnmtpvievw dldivdslep vftlgsklsk kkkkkgkss
251 saeghtdavl dlswnkl irnvl asasa dntvil w dmslgk
291 paaslavhtd kvqtlqfhp eaqtligsy dksvalydc
331 spdeshrmwr fsgqiervtw 351 nhfspchfla stddgfvynl darsdkpift
381 lna hndei sgldlssqi kgclvtas adkyvki w dilgdrp
421 slv hsr dmkmgv lfcssccpdlpfiafggakegl rv w di
461 stvssvneaf grrerlvlg arnssisgpf gsrssdtpme
501 s

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AAC-RICH protein

1 pggfqhlqqq qqqqqqqqqq qqqqqqqqtq vqqlhnqlhq qhnqqiqqqq
 51 qatqqlqtq qylsqihqq sqqsqslsnnl nsnskestni pktntqytnf
 101 dsknldlasr yfsecstkdfi
 122 gnkkkstsvawnangtkia spgsdgivrvwnfd
 155 plgnsnnnnnsntss nsknnniketi
 182 elkghdgsiekiswspknndlla spgtdkvikidvdkigkcigtvstnsenid
 235 vrwspdgdhlaidlp~~ti~~ktlkiykn geelnqvgdnnngdlilmansmgnieaykf
 301 lpkstthvkhltlygh~~ta~~s iycmefdptg kyla~~aps~~adsivslwdiedm
 351 mcvktfikst fpcrsvsfsf dgqfiaassf estieifhie
 411 ssqpihtiecgvs~~slm~~whptlpllayapesinenkdp~~si~~ rvfgyhs

Fig. 12

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BETA TRCP

1 megfscslap ptaseredcn rdepprkiit ekntlrqtklangtssmivp
 51 kqrklsanye kekelcvkyf eqwsecdave fvehlismchyqghinty
 101 lkpmlqrdfi talpargldh iaenilsyld akslcsaelv ckewyrvtst
 151 gmlwkklier mvrtdslwrg laerrgwqay lfkknppdgk tppnsfyrat
 201 ypkiiqdiet iesnwrcgr

220	hslqri <u>hcrse</u> tskgvyclayddqkivsglrdntikiwdkn tleckrv
268	lm <u>ghtgsvlclay</u> derviitgsd <u>stvrvw</u> dvntgem
305	lntli <u>hceav</u> lhrlrfnngmmvtcsk <u>drsiavw</u> dmadatditlrrv
351	lv <u>ghraav</u> nv vdfddkyivs asgdr <u>tikvwn</u> tstcefvrt
391	ln <u>ghkrgla</u> clayrdrlvvs gssdnt <u>irlw</u> diecga
427	clrv leg <u>heelyrc</u> irfdnkriivs gaydgk <u>ikvwd</u> lvaaldprapagt
475	lclrtlve <u>hsgr</u> yfrl qfdefqi vssshd <u>dt iliwd</u> flndpgla

Fig. 13

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beta-prime-cop

vks vdlhptepwmlaslyngsvcvwnhetqtlv
 51 ktfevcdlpv raakfvarkn wvvtgaddmqirvfnyntle

91 rvhmfeghsdyirciavhptqp filtssddmliklwdwdkkwscsq
 137 vfeghthyvmqivinpkdnnqfas asldrtikvwqalgssspnft
 181 leghekgvncidyysggdkpyl isgaddrlvkiwdyqnt
 221 cvqtleghaqnvscasfhpe lpiitgsedgtvriwhsst

262 yrlestlnyg mervwcvasl rgsnnvalgy degsiivklgreepamsmda
 318 ngkiiwakhs evqqanlkam gdaeikdger lplavkdmgs
 351 ceiypatiqh npngrfvvvc gdgeyiyta malrnksfgs aqefawahds
 401 seyairesns vvkifknfke kksfkpdfiga esiyggfllg vrsvnglafy
 451 dwentelirr ieiqpkhifw sdsgelvcia teesffilky lsekvlaaqe
 501 thegvtedgi edgfevlgei qeivktglwv gdcfiytssv nrlnyyvge
 551 ivtiahlprt myllgyipkd nrlylgdgel nivsysllvs vleyqtavmr
 601 rdfsmdakvl ptipkeqrtr vahflekqgf kqaaltvstd pehrfelalq
 651 lgelkiayql aveaeseqkwqlaelaisk cpfglaqecl hhaqdyggll
 701 llatasgnas mvnklaegae rdgknnvafm syflagklda clellirtgr
 751 lpeaafart ylpsqvsrvv klwrenlskv nkaaeslad pteyenlfpg
 801 lkeafvveew vkethadlwp akqyplvtpn eernvmeeak gfqpsrsaaq
 851 qeldgkpasp tpvivtsqta nkeeksllle evdldnleie didttidinld
 901 edildd

Fig. 14

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CDC4 / CDC20 protein

1 mgsfplaefp lrdipvpysy rvsggiassg svtalvtaag thrnsstakt
 51 vetedgeedi deyarkraag sgestpersd fkrvkhndhk tlhpvnlaqt
 101 gaasvdndgl hnltdisnda eklmsvddg saapstlsvn mgvashnvaa
 151 pttvnaatit gsdvsnnvns atinnpmeeg alplsptass pgtttplakt
 201 tktinnnnni adlieskdsi ispeylsdei fsainnnlph ayfknllfrl
 251 vanmdrsels dlgtlikdnl krdlitslpf eislkifnvl qfediinslg
 301 vsqnwnkiir kstslwkkll isenfvs pkg fnslniklsq kypklsqqdr
 351 lrlsflenif ilknwynokf

371	vpqrttlrgh	mtsvitclaf	ednyvitgaddkmi	<u>rvydsi</u>
411	nkkfllqlsgh	dgwwalkyahg	gilvsgst	<u>drtrvrwdi</u>
451	kkgccthvfe	ghnstvrcl	iveykniki	vtgsrdntlhv
				<u>wk</u> pkessvpdhgeehdyp
511	lvfhtpeenp	yfvglrgh	masvrtvsghg	nivvsgsydntli
				<u>vw</u> dvaqm
561	kcliyilsg	htdriystiydh		
	erkrasis	mdttiri	<u>wdl</u>	eniwnngecsyatnsasp
618	cak ilgamytl	qghtat	vgllrl	sdkflvsaaadgsir
				<u>gwdan</u>

661 dysrkfsyhh tnlisaitfy vsdnilvs gs enqfniynlr
 701 sgklvhanil kdadqiwsn fkgktlvaav ekdgqsflei ldfskaskin
 751 yvsnpvnsss sslesistsl gltrttiip

Fig. 15

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GBLP -CHLAMIDOMONAS HOMOLOG

1 maetltlratlkgh~~tnw~~taiatpldpssntllsasrdksvlwel~~er~~se
51 snygyarkalrghshf~~y~~advvi ssdgqfcltgswgtlrlwdlntgtttr
101 rfvgh~~tkd~~vlsvafs vdnrqivsgsrdktlklwntlgeck
141 ytigepeghtewyscvrfspmttnpiivsggwdkmvkvwnlt
183 ncklknnlvghhgyvntvtv spdgsllcasggkdgiamlwdlaegkrly
231 sldagdviclcfsnryw lcaatqssikiwlesksivddl
273 rpefnitskkaqvpvcvslawsadgstlysgytdgqirvwavghsl

Fig. 16

16/53

cop-1 protein

1 meeistdpvv pavkdprrts svgeganrhe nddggsggse igapdlkd
51 lcpicmqiik dafltacghs fcymciithl rnksdcpccs qhltnnqlyp
101 nflldklkk tsarhvshta spldqfreal qrgcdvsike vdnlltllae
151 rkrkmeqeea ernmqilldf lhclrkqkvd elnevqtdlq yikedinave
201 rhridlyrar drysvklrml gdpstrnaw pheknqigfn snslsirggn
251 fvgnyqnkv egkaqgsshg lpkkdalsgs dsqslnqstv smarkkriha
301 qfndlqecyl qkrrqladap nskqendksv vrregysngl adfqsvlttf
351 trysrlrvia eirhgdifhs anivssiefd rddelfatagvsrckvdf

401 ssvvnepadmcpivemstrsklsdlswnk heknhi assdyegivtvwdv
451 ttrqslmeteenekrawsvdfsrte psmlvs gsddc kvkvwctrqasvi
501 nidmkanicc vkynpgssny iavgsadhhi
531 hyydlrnisqplhvfsg hkkavsym kflsnnelasg st ds tlrlwdv
551 kdn lprvtrfrght neknfvgltnseylacgse
601 ttryvyhkei trpvtshrfg spdmddaekr qvptllvrfa
651 grvivprc

Fig. 17

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Coronin (p55)

1 mskvvrsskyrhvfaaqpkkeecyqnlkvtsawdsnyvaantryfgviwdaaggsfav

61 ipheasgkttsvplfnghksavldiafhpfnenlvgsvedcniciwgipeggltdsist

121 plqtlsgghkrkvgtisfgpvadnvavtssgdfvlktwde

161 qgknlttveghsdmitscewn hngsqivttckdkkarvfdprtnsivnev

211 vchqgvknsr aifakdkvit vgfsktsere lhiydpraft

251 tplsaaqvds asgllmpfyd adnsilylag kgdgniryye lvdespyihf

301 lsefksatpq rgldflpkrc lntseceiar glkvtpftve pisfrvprks

351 difagdiypd tyagepslta eqwsgtnae pktvslaggf vkkasavefk

401 pvvqvqegpk nekelreeye klkirvayle seivkkdaki keltn

Fig. 19

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CSTF 50kDa

1 myrtkvglkd rqqlykliis qllydgyisi anglineikp qsvcapseql
51 lhliklgmen ddtavqyaig rsdtvapgtg idlefddadvq tmspeaseye
101 tcyvtshkgp crvatysrdg qliatgsada sikildterm laksampiev
151 mmnetaqqnm

201 enhpvirtlydhvdev tclafhpte qilassr dytlklfdyskpsakra

210 fkyiqeaeml rsisfhpsgd filvgthpt lrlydintfcfvsc

256 npqghtdaicsvnyns sanmyvtgskgciklwdgvsncittf

3

0

ekahdgaevcsaifsknskiylssgkdsvallweistgrtlvrytgagls

351 grqvhrtaqvfnhte dyvllpdertislccwdsrtaerrn

391 llslghnnivrcivh sptnpgfmtcsddfrarfwyrrstt d

Fig. 20

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G-Beta 1 bovine

1 mseldqlrqe aeqlknqird arkacadatl sqitnnidpv griqmrtrrt

51 lrghlakiya mhwgtdsrll vsasqdgk- iwds

85 yttnkvhaiplrsswmtcayapsgnyvacggldnicsiynlktregnvrvsrela

141 ghtgylsccrfldd nqivtssgdttcalwdietg

174 qqtfttftghtgdvmslslap dtrlfvsgacdasaklwdvregmcra

221 tftghesdin aicffpngna fatgsddatcrlfdlradqe

261 lmtyshdnicgitsvsfsksgrlllagyddfncnvwdal kdrag

307 vlaghdnrvsclg vtddgmavatgswdsflkiwn

Fig. 21

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G-Beta- bovine (2)

1 rnqirdarka cgdstltqit agldpvgriq

31 mrtrrtlrghlakiyamhwgtdsr llvsasqdgkliids

71 egnvryttknkvhaiplrsswmtcayapsgnfvacggldnicsiyslkr

121 vsrelpghtgylsccrfldd nqiitssgdttcalwdietg161 qqtvgfaghsgdvmslslap dgrtfvsgacdasiklwdvr201 dsmcrqtfighesdinavaffp ngyafttgddatcrlfdlrada246 ellmyshdniicgitsvafsrsgrlllagyddfnciwdamkgdr291 agvlaghdnrsvclgvt ddgmavatgswdsflkiwn

Fig. 22

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G- BETA DROSOPH

1 mneldslrqe aeslknaird arkaacdtsslqaatslepigriqmrrrt

51 lrghl lakiyamhwgn dsrnlvsasqdgkli vwdshhtnk

91 haiplrsswmtcayapsgsyvacgglndmcsiynlktregnvr

135 vsrelpgh ggylsccrfl ddniqvtssgdmscgl wdietglqv

178 tsfl ghtgdvma~~sl~~a p~~q~~cktfvsgac~~da~~sakl wdiregvckq

221 tfp ghesdinavtf fpngqafatgsd~~da~~tcr lfdiradqe

261 lamys hdnii~~c~~gitsvafsksg~~rlll~~agy~~dd~~fncn vwdtm

301 kaersgilag hdnrvscig vtengmavdtgsw~~ds~~fl rvwn

Fig. 23

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G-BETA HUMAN

1	mteqmtlrgtlk <u>gh</u> ngwtqiattp	qfpdmilsasr <u>dk</u> ti <u>mw</u> kltrdet
51	nygipqralr <u>gh</u> shfvsvdvi	ssdgqfalsgsw <u>dg</u> tl <u>rl</u> <u>wdl</u> ttgtttrr
101	fv <u>gh</u> tkdvlsvaf	ssdnrqivsgsr <u>dk</u> ti <u>kl</u> wntlgvcky
141	tvqde <u>sh</u> sewscvrfsp	nssnpiivscgw <u>dk</u> lv <u>kv</u> wnla nc
183	klktnhi <u>gh</u> tgylntvtv	spdgslcasgk <u>dg</u> qam <u>l</u> <u>wdl</u>
222	negk <u>h</u> lytldggdiinalcfspnrywlcaatgpsi <u>ki</u> <u>wd</u> legkiivdel	
271	kqevistsskaeppactslawsad	gqtlfagytdnlvr <u>vw</u> qvtigr

Fig. 24

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G-Beta 2 (Human)

1 mselqlrqe aeqlrnqird arkacgdstl tqitagldpv griqmrtrrt

51 lrghlakiya mhwgtds rllvsasadgkliwdsyt

97 tnkvhaiplrsswmtcayapsgnfvacggldnicsiyslktre

151 gnvrvsrelpghtgylsccrfl ddnqiitssgdttcalwdietgqqtvgf201 aghsgdvmslslap dgrtfvsgacdasiklwdvrdsmerq241 tfighesdinavaffpn gyaf ttgsddatcrlfdlradqe281 llmyshdniicgitsvafsrsgriiagyddfncniwdam321 kgdragvlghdhrvsclgvtddgm avatgswdsflkiwn

Fig. 25

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G-Beta 4 (mouse)

1 seleqlrgeaeqlrnqiqdarkacndatlvqitsnmdsv griqmrttrrt

51 lrghlakiyamhwgydsr llvsasdgkliiwdsyttknm

91 haiplrswvmtcayapsgnyvacggldnicsiynlktregdvrvsrela

141 ghtgylsccrflddg qiitssgdttcalwdietgaqtttf181 tghsgdvmslsispd lktfvsgacdassklwdirdgmcrq221 sftghisdinavsffpsg yafatgsdatcrlfdlradqe261 lllyshdniicgitsvafsksgrrlllagydfncsywdalkggrs306 gvlaghdnrvscigv tddgmavatgswdsflriwn

Fig. 26

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GROUCHO PROTEIN DROSOPH

1 mypsvrhpa agggppagpi kftiadtlr ikeefnflqa hyhsiklece
 51 klsnektmq rhyvmyyems yglvnmhkq teiakrlntl inqllpflqa
 101 dhqqavlaqav erakavtmqe lnliigqaih aqavpggppq pmgalnpfga
 151 lgatmgllphg pagllnkppe hhrpdikptg legpaaeer lrnsvspadr
 201 ekyrtrspld iendskrrkd eklqedegek sdqdlvvdva nemeshsprp
 251 ngehvsmevr dreslngerl ekpsssgikq erppsrsqss ssrstpslkt
 301 kdmekpgtpg akartptpna aapagvnpk qmmpagpppa gypgapyarp
 351 adpyarppsd paygrppmp ydphahvrtn giphpsaltg gkpaysfhmn
 401 gegslqvpvf pddalvgvgi prharqintl shgevcavt isnptkyvyt
 451 ggkgcvkvwdisapgnknv sqldclqrdn yirsvklldgrtlivgga
 501 snlsiwdlas

511 ptpri kaelt~~tsaap~~acyal aspdskvcfscsdgniavwdl
 553 hneilvrqfa~~hntd~~gascidispdgsrlwt ggl~~ntv~~rswdlregrql

601 qqhdfssqif slgycptgdwlvagmshv evlhaskpdk yqlhlhescv
 651 lslrfaacgkwfvstgkdn lnavrtpyga sifasketss vlscdistdd
 701 kyivtgsgdk katvyeviy

Fig. 27

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GTP binding protein (squid)

1 mtselealrqeteqlknqirearkaaadtltamatavpvgriqmrtrr

51 tlrghlakiiyamhwasd srrlvssqdgklivwdgyttkn

91 vhaiprrssvmtcayapsgnyvacggldnicsiyslkr egnvrvsrel

141 pghtgylsccrfid dnqivtssgdmcalwnietgnqits

181 fgghtgdvmslslapd mrtfvsqacdasaklfdiradgick

221 qtftghesdihaityfpn gfafatgsddatcrlfdiradq

261 eigmyshdniicgitsvafsksgrrllggpyddfnrcnvwdv

301 lkqeragvlaghdnrvscl gvtedgmavatsgswdsflkiw n

Fig. 28

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IEF SSP 9306

1 madkeaafdd aveervinee ykiwkkntpf lydlvmthal ewpsltaqwl
51 pdvtrpegkd fsihrlvlgt htsdeqnhlv iasvqlpndd aqfdashyds
101 ekgefeggfgs vsgkieiek inhegevnra rympanpcii atktpssdvl
151 vfdytkhpsk pdpsgecnpd

171 lrlrghakeg yglswnpnlsg hllsasddhticlwdisav
pkegkvvdak
221 tiftghtavv edvswllhe slfgsvaddaklmiwdtrsn
261ntskpshsvdahtaevnclsfnpysefilatgsadktvalwdlrnl
307 klklhsfeshkdeifqvawsphnetilassgtdrrlnvwdls
351 kigeeqspedaedgppellfihgghtakisdf swnpne

387 pwicsvsednimqvwmelvldh

Fig. 29

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HUMAN 12.3

1	mteqmtlrgtlkghn	gwtqiattppqfpdm	ilsasr	dktiimwkl	trdet
51	nygipqralrghs	hfvsvdvvissdga	falsgsw	dgtrl	wdltt
95	gtttrrfvgh	tk dvlsvafssdn	rqi	vsgsr	dktiklwn
137	vcky tvqdes	hsewscvrfspn	ssnpiivscgw	dklykvwn	la
181	ncklktnh	ightoylntvtvs	pdgslcasggk	dggaml	wdln
222		egklytldggdii	nalcfspnrywl	caatgpsi	kiwdle
263	gkiivdelkqevist	sskaeppqctslawsadg	qtlfagytdn	lvrvwqv	tigtr

Fig. 30

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IEF -7442 - human

1 maskemfedt veervineey kiwkkntpfl ydlvmthalq wpsltvqwl
51 evtkpegkdy alhwlvlgth tsdeqnhlvv arvhipndda qfdashcdsd
101 kgefggfgsv tgkieceiki nhegevnrar ympqnphiia tktpssdlv
151 fdytkhpakp dpsgecnpl

171 rlrghakegyglswnsnlsghllsasddhtvclwdinagpkegkivdaka
221iftghsavvedvawhllheslfgsvaddqklmiwdtrst
261 tskpshlvdahtaevncsfnpyselilatgsadktvalwdlrnlklklh
311 tfeshkdeifqvhwsphneti lassgtddrrlnvwdlskigeeqsaedaed
361 gpellfihgghatakisdfswnpnepwvicsvsegnimqiwwmaeniynd

411 eesdvttse egqgs

Fig. 31

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insulin-like growth factor binding protein complex

1 malrkggla allllswal gprslegadp gtpgeaegpa cpaacvcsyd
51 ddadelsvfc ssrnltrlpd gvpgggtqalw ldgnnlssvp paafqnlssl
101 gflnlqggql gslepqallg lenlchlhle rnqlrslalg

141 tfahtp[alaslglennrlsrledgl]feglgslw~~dl~~nlgwn slavlldaaf
rglgslrelv

201 lagnrlayla palfsglael reldlsrnl raikanvfvq lprlaklyld
251 rnliaavapg aflglkalrw ldlsnrvag lledtfpgll glrvlrslhn
301 aiaslrprt f kdlhfleelq lghnrirqla ersfeglgql evltldhnql
351 qevkagaflg ltnvavmnl gncrlnlpeq vfrglgklhs lhlegscigr
401 irphtftgls glrrlflkdn glvgieeqsl wglaelleld ltsnqlthlp
451 hrlfqglgkl eylllsrnl aelpadalgp lqrafwldvs hnrlealps

501 llaplgrlry lslnnsrlt ftpqppgler lwlegnpwdc gcplkalrdf
551 alqnpsavpr fvqaicegdd cappaytynn itcasppevv gldlrdlse
601 hfapc

Fig. 32

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insulin like growth factor binding protein complex - rat

1 malrtggpal vlllafwval gpchlqgtdp gasadaegpq cpvactcshd
51 dytdelsvfc ssknlthlpd dipvstralw ldgnnlssip saafqnlssl
101 dflnlqagswl rslepqallg lqnlyylhle rnnrlnlavg

141 lft~~htpslasls~~ssnllgrleeglfagls~~hlw~~dlnlgwn

181 slvvlpdtvf aglgnlhelv
201 lagnkltylq palfcglgel reldlsrnl rsvkanvfvh lprlqklyld
251 rnlitavapg aflgmkalrw ldlsnrvag lmedtfpgll glhvlrlahn
301 aiaslrprt看 kdlhfleelq lghnrirqlg ertfeglgql evltlndnqi
351 tevrvgafsg lfnvavmnl s gncrlslper vfagldklhs lhlehscigh
401 vrlhtfagls glrrlflrdn sissieeqsl aglselleld lttlrlthlp
451 rqlfaglgghl eylllsynql ttlsaevlgp lqrafwldis
491 hnhletlaeglfsslgrvrylslnnslqtfsppqglerlwl~~danp~~w~~dc~~s
541 cplkalrdfa lqnpgvvprf vqtvceggdc qpvtyynnlt cagpanvsgl
dlrdvsethf
601 vhc

Fig. 33

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LIS1 (human)

1 mvlqrqrde lnraiadylr sngyeeaysv fkkeaeldvn eeldkkyagl

51 lekwtsvir lqkkvmeles klineakeeft sggplgqkrd pkewiprppe

101 kyalsghrspvtrvifhpfsvmsasedatikiywdyetg151 dfertlkghtdsvqdisfdhsgkllascsadmtiklwdfagfecir191 tmhghdhnyssvaimpngdhivsasrdktikmwevqtgycvktf241 tghrewrmvrpnqdgltiascsndqtvryvwvatkecka

291 elrehevveciswapessy

311 ssiseatgsetkksgkpgp flsgsrdkt kmwdvstgmc351 lmtlvghdnwrgvlfhsggkfilscaddktlrvwdyknk391 rcmktlnahehfytsldfhktapyvvtgsvdqtvkwecr

Fig. 34

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MD6

1 merkdftwl dnisvtflsl mdlqknetld hlislsgavq lrhlsnnlet
 51 llkrdfklkl plelsfyllk wldpqtlitc clvskqrnkvl isactevwqt
 101 acknlgwqid dsvqdsllhwk kvylkailrm kqledheafe

141	tssli <u>gh</u> sarvyalyyk	dglletgsd <u>dl</u> sak <u>lwd</u> vstgqc
181	vygiqth <u>tda</u> avkfde	qklvtgsf <u>dt</u> vac <u>wew</u> ssgart
220	qhfr <u>gh</u> tgavfsvdysdel	dilvsgs <u>ad</u> favkv <u>wal</u> sagtc
261	lntlt <u>gh</u> tewtkvvlqckvksslhspgdyill	sakyeiki <u>wpi</u> grei

301 nckclktlsv sedrsiclap rlfhdgkyiv cssalglyaw
 351dfasydilrv iktpevanla llgfgdvfal lfdnhylyim dlrteslir
 401wplpeyrksk rgtsflager pg

Fig. 35

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MSL1

1 mncakdith eassipidlq eryshwkknt kllydylntn stkwpsltcq
51 ffpdltdtsd ehrillssft ssqkpedeti yiskistlgh ikwsslnnfd
101 mdemefkpen strfpskhlv ndisiffpng ecnrarylpq npdiagass
151 dgaiyifdrft khgstrirqs kishpfetkl fgshgviqdv eamdtssadi
201 neatslawnl qqealllssh sngqvqvwdi kqyshenpii dlolvsinsd
251 gtavndvtwm pthdslfaac tegnavslld lrtkkekqls

291 nrekhdggvnsrfrn yknslllasadsngrlnlwdirnmm
331 kspiatmehgtsvstlewspnfdtvlatagedgl vklwdsceetifth
381 gghmlgvndisw dahdpwlmcsvandn svhiwkpagnlv ghs

Fig. 36

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MUS MUSCULUS PROTEIN

1 msshesyt na aetpenisil sclgetsgal vdtktisdik tmdprvsltp
 51 ssdvtgteds svltpqstdv nsdtsyqgye gdddeedde ddkdgsnlp
 101 sledsdnfis clensyipqn vengevveeq slgrrfhpye leagevveeq
 151 gggslyfpye leagevveeq nvqnlfhrye leagevveeq vvqsmfpye
 201 leagevveae evqgffqrye learevigaa ggqglshrhyg leggevveat
 251 avrrliqhhe leegedvddq eessemheet sedseeydi eddslidewi
 301 aletsplprp rwnvisalrd rqlgssgrfv yeacgarlfv qrfv

351 lehvfeghsqdvntvh	fnqhgt lasgsddlkviyvdwllkkrsvln
----------------------	---------------------------------

Fig. 37A

37 / 53

391 fdsghknnilqakflpncnd ailamcgrdg qvrvaqlsav
 401 agthmtkrlv khggashrlglepdsprfl tsgedavvfn
 451 idlrqahpas kllvikdgdg kvglytvfvn
 501 panvyqfavg gdaqfmriyd qrkidenvnn gvlkkfcphh llssdypahi
 551 tslmysydgdt eilasyn ded iyifnssdsd gaayakrykg hrnnstvkgv
 601 yfygrprsefv

611 msgsdcg hif iweksscqv qfleadeegt incidshpylpvldssgldheykiwspiae

671 pskklaglkn vikinklkrd nftlrhtslf
 701nnsmlcflms hvtqsnysgrswrgirinagg gdfsdsssss eetnqes

Fig. 37B

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ORF RB1

1 mnqcakdith eassipidlqeryshwkknt klydylnn stkwpstcq
51 ffpdltdtsd ehrillssft ssqkpedeti yiskistlgghikwsslnnfd
101 mdemefkpen strfpskhv ndisiffpng ecnrarylpq npdiagass
151 dgaiyifdrf khgstirqs kishpfetkl fgshgviadv eamtssadi
201 neatslawnl qgeallssh sngqvqvdi kayshenpii dlplvsinsd
251 gtavndvtwm pthdslaac tegnavsld lrtkkekls

291 nrekhdggvnsrnfnykn slilasadsngrlnlwdirmn
331 kspiatmehgtsvstlewsfnfdtvlataqgedg lyklwdsceetifh
381 gghmlgvndiswdah dpwlmcsyandn syhiwkpagnlvghs

Fig. 38

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Periodic Trp protein.

1 misatnwvpr gfssefpeky vlddeeveri nqlaqlnldd akatleeaeg
 51 esgveddaat gssnklkdql didddlkeyn leeyddeeia dneggkdvsm
 101 fpglsndsdv kfhegekged pyislpnqed sqeekqelqv ypsdnlvlaa
 151 rteddvsyld iyvyddgagf hssdipveeg deadpdvarg lvrpalyvh
 201 hdlmlpafpl cvewldykv gsnseeaanya aigtfdpqie iwnldcvdka
 251 fpdmilgepl dnsmvslksk

271 kkkkksktgh itthhtdavl smahnkyfrsvlastsadhtv klw~~dl~~nsn
 321 aarslasihs nk~~h~~vssewhmlngsilltggysrvaltd~~vr~~isdesqmskywsamagee

381 ietvtfasen iilcgtdsgn vysfdirne nrkpvwtlka
 421 hdagistlcs nkfigmmst gamgektvkl
 451 wkfplddatn tkgpsmvlsr dfdvgnvlts sfapdievag tmviggvnkv
 501 lklwdvftnr svrksfksel envqarakee aqkigkssri arkytsndnp
 551 dtvitiddqg edeeereggd ehddma

Fig. 39

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PLAP

1 mhymsghsnf vsyvciipss diyphgliat ggndhnicif sldspmplyi

51 lk~~gh~~kdvtvcslssgkf gtlsgswdttakvw!ndkcmmtl

91 q~~gh~~taavwavkilpeaglm!tgsadktiklwkagrcertf

131 l~~gh~~edcvrglails eteflscandasirrwaitgeclevy

171 f~~gh~~tnyiysisvfpnskdfyttaedrs!riwkhgecaqti

211 rlpaqsiwcc cvlengdivv gasdgiirvf teseertasa

251 eeikaslsre spliakvltt eppiitpvr tlpcrvtrsm issclsrivs

301 tslstdshl titalhlflt tttte

Fig. 40

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RETINOBLASTOMA BINDING PROTEIN - HUMAN

1 madkeaafdd aveervinee ykiwkntpf lydlvmthal ewpsltaqwl
 51 pdvtrpegkd fsihrlvlgt htsdeqnhlv iasvqlpndd aqfdashyds
 101 ekgefsgfgs vsgkieiek inhegevnra rymqnpccii atktppssdvl
 151 vfdytkhpsk pdpsgecnpd
 171 lrlrghqkegyglswnpn lsghl~~l~~ sasddhticl~~wd~~isavpkegkvvdak
 221 tiftgh~~h~~tavvedvswlll hslf~~g~~svaddqklmi~~wd~~trsn
 261 ntskps~~h~~svd~~h~~taevnc~~l~~sfnpys~~e~~fil~~g~~tg~~s~~ad~~k~~ktval~~wd~~lrnlklkl
 311 hsfesh~~k~~deifqvqwsph netil~~g~~ssgtd~~r~~rrlnv~~wd~~l~~s~~kigeeqspedaedgppell
 374 fihgg~~h~~takis~~d~~fswnp~~n~~epw vic~~s~~vsed~~n~~imqv~~wd~~maeni~~y~~nded~~p~~egsvdpegqgs

Fig. 41

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S253 PROTEIN

1 mfkststls ydetpnsneg drnatpvnk eksqtkhlni pgdrsrhssi
 51 adskrsssry dggysadiip aqlrfidnid ygtrlrktlh rnsvvsngyn
 101 klsendrwyf dlfdkyfen yleptyiki fkkkegleaf drmflaqelk
 151 ipdvykstty agepavanse lfknsiccct fshdgkymvi gckdgsllhw
 201 kvinspvkrs emgrseksvs asranslkiq rhlasisshn gsisndlkp
 251 sdqfegpskq lhlyapvfys

271 dvfrvmeha dildanw skngflitasmdktoklwhper
 311 kyslktfvhpdvtsaiffpnddrfiitgcldhrcrlwsi

351 ldnevsyafd ckdltstlt sppggeytii gtfngyiyvl lthglkfvs
 401 fhvskstqg ttknsfhpss eygkvqhgr itglqcffsk vdknlrlivt
 451 tndskiqifd lnekkplelf kgfqsqssrh rgqflmmkne pvvftgsddh
 501 wfytwkmsf nlsaemncta phrkkrlsgs mslkgllriv snkstndekl
 551 tetsnqsssh tftnssknvl qtqtvgsqai knnhyisfha hnsptvcasi
 601 apdvaiknls lsndlifelt sayfkemgn ysesketcdn kpnhpvtetg
 651 gfssnlsnvv nnvgtilitt dsqglirvfr tdilpeirkk iekfheynl
 701 fhleaagkin nhnndsilen rmderssted nefsttppsn thnsrpsdhf
 751 celhpnnspv isgmprasa ifknsifnks ngsfislksr seststsvfg
 801 phdiprvstt ypklkcdvcn gsnfecaskn piaggdsgft cadcgtilnn
 851 fr

Fig. 42

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SOF1

1 mkiktikrsa ddvvpvkstq esqmprnlp elhpferare ytkalnatkl

51 ermfpkpfvgalgyghrdgvy aiaknygslnklatqsdagvikywnmstr

101 eefvsfkahyglvtglcvtpqprfhdkkpdllksqnfmlsqsdgktvklwsiinvddysnkns

161 sdndsvtneeqlirtfdgesafqgidshrenstfdtggakihlwdvnrk

211 pvsdlswgad nitslknfn etdilastgs dnsivlydlr tnsptqkivq tmrtnaicwn

271 pmeafnfvta nedhnayyyd mrnlrsrlnv fkdhsavmd vdfsptgdei vtgsydxsir

331 iyktnhghsreihtkrmqhvf vkysmdskyiisgddggnvrlwrskaw

381 ersnvkttre knkleydekl kerfrhmpei krisrhrhvp qvikkaqeik

431 nielssikrr eanerrtrkdmypyiserkkq ivgtvhkyed sgrdrkrke ddkrdtqek

Fig. 43

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STE4 - YEAST

1 maahqmdsit ysnvtaqyi qpasldisa vedeiqnie aarqeskqlh
51 aqinkakhki qdaslfqman kvtsltknki nlkpnlv

89 kghnnkisdfwrsk rilsasqdgfmliwdsasglqnai

131 pldsqwlscaispsstlvasaglnnnctiyrvskenrva

171 qnvasifkghncyisdieft dnahiltasgdm~~tc~~alwdip
211 kakrvreysdhlgdvlalapeepnlenssntfascgsdgytyi~~wd~~srsp

261 savqsfyvndsdinalrffkdgmsivagsd ngainmydlr
301 sdcslatfslfrgyeertptptymaanmey ntaqspqtlk

341 stsssyldnqgvvsldfsasgrlm~~ysc~~tydigcv~~wd~~vlk
381 geivgklegghgrvtgvrsspdglavctgswdstmki~~w~~sp gya

Fig. 44

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TRANSCRIPTION FACTOR TIIF

1 mslevsning gngtqlshdk relcllklk kkyqlkstee llcqeanvss
51 velseised vqqlgavlg agdanrerkh vqspaaghkq savteanaae
101 elakfidds fdaqhyeqay kelrtfveds ldiykhelsm vlypilvqi
151 fki lasglre kakefiek yk cdl dgyyieg lfnllllskp eellendlw
201 ameqdkfvir msrdshslfk rhiqdrreqv vadivskylh fdtyegmarn
251 klqcvatags hlgeakraqdn kmrvygyllk evdfqtlttp apapeeeddd
301 pdapdrpkkk kpkkdpllsk kksdnpaps idriplpelk dsdkllklka
351 lreaskrlal skdqlpsavfytvln

Fig. 45A

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376 shqgvtcaeisddstm lacgfgdssvriwsltpanvrtlkdds
 ▲ lreldkesadi

431 nvrmlddrsgevtrs lmghtgpyrcafapemnl lscsedstirlwsl l

481 twscvvtyrghvypwvdvrfaphgyyfvscsydktarlwatdsnqalrvf

531 vghlsdvdcvqfhpnsnyvqatgssdrtyrlwdnmtgqsvr

571 lmtghkqsvsslafsaagrylqsgsvdhni i iwdl sngsl

611 vtlllrhtstvtttitfsrdgtvlqaaagldnnltlwdfhkv

651 tedyisnhit vshhqadende dvytmrtfps knspfvslhf trrnllmcvg
 701 l fks

Fig. 45B

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TUP1

1 mtasvsntqn klnellldair qeflqvsqea ntyrlqnqkd ydfknnqqla
 51 emqqirntvy elelthrkmk dayeaeikh1 klgleqrdhq iasltvqqqq
 101 qqqqqqqvqq hlqqqqqqla aasasvpvaa qppattsata tpaantttgs
 151 psafpvqasr pnlvgslpt tt1pvssna qqqlpqqqla qqqlqqqqpp
 201 pqvsvaplsn taingsptsk etttlpsvka pestlketep ennntskind
 251 tgsattat1t1 tateteikpk eedatraslh qdhylvpynq ranhskpipp
 301 flldldsqs1 pdalkkatnd yyilypalp reidvelhks ldhtsvvccv
 351 kfsndgeyla tgcnkttavy rvsdgs1var lsddsaannh rnsitenntt
 401 tstdnntmtt tttttittta mtsaaelakd venlntsssp

441 ssdly1rsvcfspdgkflatgaedrl1riw1dienrkivmi
 481 lqgheqdiysldyfpsgdklvsgsgdr1vriw1l1rtgqcs
 521 ltlsiedgvttvavspgdgkyiaagsl1dravrvwdsetgflverldsene
 571 sgtghkds1vsvvft1rdgqsvvsgsl1drsvklwnlqnannksdsktpnsg
 621 tcevytighkdfvlsvattqndeyilsgsk1drgvlfwdkk

661 sgnpllm1ag hrnsvisvav angssl1gpey nvfatgsgdc
 701 kariwkykki apn

Fig. 46

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TUP1 HOMOLOG

1 msqkqstnqn qngthqapqv knqrtnnaag ansgqapqaa sqgqsqqqgr
 51 sngpfsasdl nrivleylnk kgyhrteaml raesgrtltp qnkqspantk
 101 tgkfpeqssi ppnpghtakp isnptnlssk rdaeggivss grleglnape
 151 nyiraysmlk nwdssleiy kpelsyimyp ifiylflnlv aknpvyarrf
 201 fdrfspdfkd fhgseinrlf svnsidhike nevasafqsh kyritmsktt
 251 lnlllyflne nesiggslii svinqlhdpn ivesvtarek ladgikvlsd
 301 sengngkqnl emnsvpvklg pfpkdeefvk eietelkikd dqekqlnaqt
 351 agdnysgann rtllqeykam nnekfkdtg dddkdkikdk iakdeekkes
 401 elkvdgekdd snlsspardi lplppktald lkleiqkvke sdaikldnl
 451 qlalpsvcmy

461 tfqntnkdmcldfsadcriaaag fadsyikiwsl dgsslnnpnialnnn
 511 dkdedptcktlvghsgtvystsf spdnkyllsgsedkt vrlwsmdthtal
 561 vsykg~~h~~nhpvwdvs fsplghyfatashdqt arlwscdhiy
 601 plrifag~~h~~lndvdcvs fhpngcyvftgssdkt crmwdvst
 641 gdsvrflg~~h~~tapvisi avcpdgrwltsgsedgi invwdigtgkr
 686 lkqmrgh~~g~~knaiyslsyskegnvltisggadht vrvwdlkkattep

731 saepdeffig ylgdvtasin qdikeygrrr tviptsdlva
 771 sfytkktpvf kvkfsrsnla laggafpr

Fig. 47

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YCU7

1 mvrfrgkel aattfnghrd yvmgaffshd qekiytvskd gavfwefk
51 rpsddddnes edddkqeevd iskyswritk khffyanqak vkcvtfhpat
101 rllavgftsg efrlydlpdf tliqqlsmgq npvntvsvnq tgewlafgss
151 klgqllvyew

161 qsesyilkqagghfdstns lay spdgsvvtasedgkikvwd
202 itsgfclatfeehtssvta vqfakrgqvmfssldgtvrawdli
251 ryrnfrtftgteriqfncldvpsgevcagsldnfdih vwsvqt
291 gqllldalsghegpvscl sfsqensvlasaswdktiriwsi

341 fgrsqavepi evysdvlals mrpdgkevav stlkgqisif niedakqvg
391 idcrkdiisg rfnqdrftakilndpnflq yitvlmwll wlvviitpfv
431 ymmfqmksc

Fig. 48

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YCW2 PROTEIN

1 mstlippsk kqkkeaqldr evaiipkdlp nvsikfqald tgdnvvgalr
 51 vpgaiseqal eellnqlngt sddpvpytfs ctiaggkasd pvktiditdn
 101 lysslikpgy nstedqitll ytpravfkvk

131	pvtrsssaia <u>gh</u> stilcsafaph	tssrmvtgagdn tariw dcdtqtpmh
181	tlk <u>gh</u> ynwlcvswhp	dgeviatgsm dn tirlw dpk sgqc
221	lgdalr <u>gh</u> skwitslswepihlvkpgskprlasssk dgtikiw dtvsrvc	
271	qytms <u>gh</u> tnsvscvkwggag	llysgsh drtvrw dinsag

311 rcinilksha hwnhlslst dylrigafd htgkkpstpe

351	eaqkkalenyekickknngse	emmvtdasdytmf lwn plkstkpia rmtg
401	hqklvn <u>h</u> vafspdgr	yivsasf dn sikl wdgr
441	dgkfistfr <u>gh</u> iasvyqvawssdc	rllvscsk dt tlkv w dv
481	rtrklsvdlpgiktklyvdw	svdgkrvcsggk dkm vr lw th

Fig. 49

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Fig. 50

YKL525

1 mfkststls ydetpnsneg drnatpvnk eksqtkhl ni pgdrsrhssi
 51 adskrsssry dggysadiip aqlrfidnid ygtrlrktlh rnsvvsngyn
 101 klsendrwyf dlfdkyfen yleeptyiki fkkkegleqf drmflaqelk
 151 ipdvkstty

161 qgepavanselfknsiccct fshdgkymvi gckdgsllhwk

202 vinspvkrs emgrseksvs asranslkiq rhlasissn gsissndlkp

251 sdqfegpskqlhlyapvfysdvf rvmehaldildanwskngflitasmd

301 ktaklwhperkyslktfvhpdvtsaiffpnddrfiitgcldhrcrlwsi

351 ldnevsyafd ckdltstlt sppggeytii gtfngyiyvl lthglkfvs
 401 fhvskstqg ttnsfhpss eygkvqhgpr itglqcffsk vdknlrlivt
 451 tndskiqifd lnekkplelf kgfsgssrh rgqflmmkne pvvftgsddh
 501 wfytwkmsf nlsaemncta phrkkrlsgs mslkgllriv snkstndekl
 551 tetsnqsssh tftnssknvl qtqtvgsqai knnhyisfha hnsptvcasi
 601 apdvaiknls lsndlifelt sayfkemgqn ysesketcdn kpnhpvtetg
 651 gfssnlsnvv nnvgtlitt dsqglirvfr tdilpeirkk iiekfheynd
 701 fhleaagkin nhnndsilen rmderssted nefsttppsn thnsrpsdhf
 751 celhpnnsnv isgmprasa ifknsifnks ngsfislksr seststsvfg
 801 phdiprvstt ypklkcdvcn gsnfecaskn piaggdsgft cadcgtilnn
 851 fr

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yrb 1410 yeast

1 msqkqstnqn qngthqpqv knqrtnnaag ansgqapqaa sqgqsqaagr
51 sngpfsasdl nrivleylnk kgyhrteaml raesgrtltp qnkqspantk
101 tgkfpeqssi ppnpgktakp isnptnlssk rdaeggivss grleglnape
151 nyiraysmlk nwdssleiy kpelsyimyp ifiylflnlv aknpvyarrf
201 fdrfspdfkd fhgseinrlf svnsidhike nevasafqsh kyritmskt
251 lnlllyflne nesiggslii svinqhldpn ivesvtarek ladgikvlsd
301 sengngkqnl emnsvpvklg pfpkdeefvk eietelkikd dqekqlnqqt
351 agdnysgann rtilqeykam nnekfkdtg dddkdkikdk iakdeekkes
401 elkvdgekkd snlsspardi lplppktald lkleiqkvke srdaikldnl
451 qlalpsvcmy tfqntnkams cldfsddcri aaagfqdsyi kiwslgdssl
501 nnpnialnnn dkdedptckt lvghsgtvys tsfspdnkyl lsgsedktvr

Fig. 51A

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551 lwsmdtthalvsyghnnhpvdvs fsplghyfatahshdqtarlwscdhiy
601 plrifaghlndvdcvs fhpngcyvftgssdktrmwdvst
641 gdsvrflghhtapvisiav cpdgrwlstgsgdgiinvwdigtgkrkqmr
691 ghgknaiyslsyskegnvlisggadhtvrvwdlkkattep
731 saepdepfig ylgdvtasingdikeygrrr tyiptsdlva sfytkktpvf
kvkfsrsnla laggafpr

Fig. 51B